



# STIC Search Report

## Biotech-Chem Library

### STIC Database Tracking Number: 10/654737

**TO:** Franco M Salvoza  
**Location:** REM/3B49/3C18  
**Art Unit:** 1648  
**Friday, September 23, 2005**

**Case Serial Number:** 10/654737

**From:** Paul Schulwitz  
**Location:** Biotech-Chem Library  
**REM-1A65**  
**Phone:** 571-272-2527

**Paul.schulwitz@uspto.gov**

### Search Notes

Examiner Salvoza,

Please review the attached search results.  
If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
REM-1A65  
571-272-2527

166505

**From:** Page, Thurman  
**Sent:** Wednesday, September 21, 2005 4:08 PM  
**To:** STIC-Biotech/ChemLib; Salvoza, Franco  
**Cc:** Page, Thurman  
**Subject:** FW: rush sequence search request  
  
**Importance:** High

## RUSH SEARCH APPROVED

-----Original Message-----

**From:** Salvoza, Franco  
**Sent:** Wednesday, September 21, 2005 3:59 PM  
**To:** Page, Thurman  
**Subject:** rush sequence search request

Mr. Page,

I'd like to kindly request a rush sequence search for application 10/654,737. It is an overdue amendment which was transferred to me (a new junior examiner) from an examiner that has since left the USPTO.

I am interested in an updated search for SEQ ID NOs: 5 and 6 for this application as well as an interference search to prepare it for allowance.

thank you for your time and consideration.

best regards,

Franco Salvoza

Examiner Franco Salvoza  
 AU1648  
 REM 3B49  
 x8410

RECEIVED  
 SEP 21 2005  
 STIC/CHEN, DIVISION  
 (STIC)

\*\*\*\*\*  
 Searcher: \_\_\_\_\_  
 Searcher Phone: \_\_\_\_\_  
 Date Searcher Picked up: \_\_\_\_\_  
 Date completed: 9/23  
 Searcher Prep Time: \_\_\_\_\_  
 Online Time: \_\_\_\_\_

\*\*\*\*\*  
 Type of Search  
 NA# \_\_\_\_\_ AA# \_\_\_\_\_  
 S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
 Encode/Transl: \_\_\_\_\_  
 Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
 Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
 Vendors and cost where applicable  
 STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 QUESTEL/ORBIT: \_\_\_\_\_  
 LEXIS/NEXIS: \_\_\_\_\_  
 SEQUENCE SYSTEM: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (Specify): \_\_\_\_\_

GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2005, 21:28:42 ; Search time 156.61 Seconds  
(without alignments)

568.004 Million cell updates/sec  
Title: US-10-654-737-5  
Perfect score: 1172

Sequence: 1 MDPNNTYSSPQYDCFLWHRK.....RPPLTPKQKRMARTIREV 230

Scoring table: BLOSUM62  
Gapext 0.5

Searched: 2105692 seqs, 38676381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: GeneseqP980s:\*
- 2: GeneseqP1990s:\*
- 3: GeneseqP2000s:\*
- 4: GeneseqP2001s:\*
- 5: GeneseqP2002s:\*
- 6: GeneseqP2003as:\*
- 7: GeneseqP2003bs:\*
- 8: GeneseqP2004s:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1140	97.3	237	5	AAE23116		Aae23116 Influenza
2	1107	94.5	230	8	ADo14171		Ado14171 Influenza
3	1019	92.1	230	8	ADo14175		Ado14175 Influenza
4	1078	92.0	217	8	ADo14178		Ado14178 Influenza
5	1075	91.7	237	5	ABo5772		Abbo5772 Influenza
6	1057	90.2	227	8	ADo14179		Ado14179 Influenza
7	1054	89.9	230	2	AAW0522		Aaw0522 Non-struct
8	1052	89.8	230	4	AAE09027		Aae09027 Equine in
9	1006	89.8	230	4	AAE09029		Aae09029 Equine in
10	1050	89.6	227	8	ADo14177		Ado14177 Influenza
11	1047	89.3	230	8	ADo14174		Ado14174 Influenza
12	1046	89.2	227	8	ADo14180		Ado14180 Influenza
13	1035	88.3	230	8	ADo14176		Ado14176 Influenza
14	1021	87.1	230	8	ADo14183		Ado14183 Influenza
15	1006	85.8	202	8	ADo14184		Ado14184 Influenza
16	844	72.0	230	8	ADo14182		Ado14182 Influenza
17	835	69.4	173	8	ADo14173		Ado14173 Influenza
18	813	69.4	173	9	AAE09028		Aae09028 Equine in
19	424	36.2	246	2	AAW12714		Aaw12714 Flu NS1-H
20	415.5	35.5	246	2	ABU71886		Abu71886 Human pro
21	412	35.2	344	4	ADo14186		Ado14186 Human pro
22	411	35.1	124	8	ADo14182		Ado14182 Influenza
23	407.5	34.8	231	2	AAW20301		Aaw20301 Val1(1) to
24	406.5	34.7	309	2	AAE13175		Aae13175 NS1-81-RL
25	406.5	34.7	319	2	AAR07945		Aar07945 NS181RLPA

#### ALIGNMENTS

RESULT 1  
AAE23116 standard; protein; 237 AA.

ID AAE23116;

XX AAE23116;

AC AC;

DT DT;

XX 21-AUG-2002 (first entry)

DE Influenza A virus/singapore/1/57/ca NS1 mutant protein.

XX Attenuated influenza vaccine; prophylactic; therapeutic; infection; viricide; mutant; muclein; NS1 protein.

XX Influenza A virus.

OS Synthetic.

OS

XX WO2002241876-A2.

XX 28-MAR-2002.

PD XX

XX 25-SEP-2001; 2001WO-EPO11087.

PF XX

PR XX

PA XX

XX (POLY-) POLYMYR SCI IMMUNOBIOLOGISCHE FORSCHUNG.

PI Karlinger H, Egorov A, Ferko B, Romanova J, Katinger D;

XX DR WPI; 2002-416282/44.

DR N-PSDB; AAD37061.

XX Example 4; Page 62-63; 90pp; English.

XX The present invention relates to a method for isolating viruses from various sources and for producing live attenuated influenza vaccines in a serum-free African Green monkey kidney (vero) cell culture under conditions where alterations in the surface antigens of the virus due to adaptive selection are minimised or prevented. The method is useful for the manufacture of whole-virus vaccine, preferably attenuated live vaccine. It is useful for prophylactic or therapeutic administration against viral infection, preferably influenza virus infections. The present sequence is Influenza A virus/singapore/1/57/ca (cold adapted) NS1 mutant protein. This sequence is used in the exemplification of the invention.

xx Sequence 237 AA;  
 SQ Score 1140; DB 5; Length 237;  
 Best Local Similarity 96.1%; Fred. No. 1.2e-118;  
 Matches 221; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 MDPNTVSSFOVDCFLWHVRKRAQDQELGDAFLDRDQKSLRGRGSTLGGINIEATAIR 60  
 Db 1 MDPNTVSSFOVDCFLWHVRKRAQDQELGDAFLDRDQKSLRGRGSTLGGINIEATAIR 60  
 Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTEMSRDWFLMLPKOKVAGPLCIRND 120  
 Db 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTEMSRDWFLMLPKOKVAGPLCIRND 120  
 Qy 121 QAIMDKSIIKANFSVTFDRLTLLRAFFEGAVGEISPLPSLGHITNEDIKNAIGV 180  
 Db 121 QAIMDKNIIKANFSVTFDRLTLLRAFFEGAVGEISPLPSLGHITNEDIKNAIGV 180  
 Qy 181 LIGGLEWNNTTVRSKTLQRFAWSNSNENGRPLTPKQGRKMARMTIRSKV 230  
 Db 181 LIGGLEWNNTTVRSKTLQRFAWSNSNENGRPLTPKQGRKMARMTIRSKV 230

RESULT 2  
 ADO14171 ID ADO14171 standard; protein; 230 AA.  
 AC ADO14171;  
 XX DT 12-AUG-2004 (first entry)  
 XX DB Influenza A virus non-structural protein (NS)-1 #1.  
 XX OS influenza inhibitor; non-structural protein-1; NS1;  
 KW double-stranded RNA; dsRNA; binding domain; virucide;  
 KW double-stranded-RNA-activated protein kinase; phosphorylation;  
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
 KW viral protein replication; screening method; infection.  
 XX OS Influenza A virus; A/Udorn/307/72 (H3N2).  
 XX PN WO2004043404-A2.  
 XX PD 27-MAY-2004.  
 XX 13-NOV-2003; 2003WO-US036292.  
 XX 13-NOV-2003; 2002US-042561P.  
 PR 10-JUN-2003; 2003US-0477453P.  
 XX PA (RUTP ) UNIV RUTGERS STATE NEW JERSEY.  
 XX PI Montelione GT, Krug RM;  
 XX DR 2004-420083/39.  
 XX PT Identifying agents useful for treating influenza virus infection  
 PT comprises identifying compounds that inhibit binding between influenza  
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
 PT the protein.  
 XX Disclosure; Page 11; 92PP; English.

XX This invention relates to a novel method of identifying an inhibitor of  
 CC influenza virus which comprises testing candidate compounds for their  
 CC ability to reduce the extent of binding between influenza virus non-  
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
 CC domain and a dsRNA that binds the protein. The invention may be useful  
 CC for the production of compounds with a virucide activity acting as  
 CC inhibitors of binding between influenza virus non-structural protein-1  
 CC (NS1) and double-stranded RNA. It is possible that binding of double-  
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA

CC -activated protein kinase to remain in an inactive state so that it does  
 CC not catalyse the phosphorylation of translation inhibition factor  
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
 CC replication. The invention is useful as a high throughput screening  
 CC method for identifying compounds having inhibitory activity against  
 CC influenza virus. Compounds identified are useful in treating animals,  
 CC including human infected with influenza virus. The present sequence is  
 CC that of an influenza virus non-structural (NS)-1 protein which is related  
 CC to the method of the invention.

XX Sequence 230 AA;  
 SQ Score 1107; DB 8; Length 230;  
 Best Local Similarity 93.5%; Pred. No. 5.9e-115;  
 Matches 215; Conservative 10; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 MDPNTVSSFOVDCFLWHVRKRAQDQELGDAFLDRDQKSLRGRGSTLGGINIEATAIR 60  
 Db 1 MDPNTVSSFOVDCFLWHVRKRAQDQELGDAFLDRDQKSLRGRGSTLGGINIEATAIR 60  
 Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTEMSRDWFLMLPKOKVAGPLCIRND 120  
 Db 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTEMSRDWFLMLPKOKVAGPLCIRND 120  
 Qy 121 QAIMDKSIIKANFSVTFDRLTLLRAFFEGAVGEISPLPSLGHITNEDIKNAIGV 180  
 Db 121 QAIMDKNIIKANFSVTFDRLTLLRAFFEGAVGEISPLPSLGHITNEDIKNAIGV 180  
 Qy 181 LIGGLEWNNTTVRSKTLQRFAWSNSNENGRPLTPKQGRKMARMTIRSKV 230  
 Db 181 LIGGLEWNNTTVRSKTLQRFAWSNSNENGRPLTPKQGRKMARMTIRSKV 230

RESULT 3  
 ADO14175 ID ADO14175 standard; protein; 230 AA.  
 AC ADO14175;  
 XX DT 12-AUG-2004 (first entry)  
 XX OS Influenza A virus non-structural protein (NS)-1 #5.  
 DE XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
 KW XX double-stranded RNA; dsRNA; binding domain; virucide;  
 KW XX double-stranded-RNA-activated protein kinase; phosphorylation;  
 KW XX double-stranded-RNA-activated protein kinase; phosphorylation;  
 KW XX translation inhibition factor; eIF2alpha; viral protein synthesis;  
 KW XX viral protein replication; screening method; infection.  
 OS XX  
 PN WO004043404-A2.  
 XX PD 27-MAY-2004.  
 XX PP 13-NOV-2003; 2003WO-US036292.  
 XX PR 13-NOV-2003; 2002US-042561P.  
 PR 10-JUN-2003; 2003US-0477453P.  
 XX PA (RUTP ) UNIV RUTGERS STATE NEW JERSEY.  
 XX PI Montelione GT, Krug RM;  
 XX DR 2004-420083/39.  
 XX PP 13-NOV-2003; 2003WO-US036292.  
 XX PR 13-NOV-2002; 2002US-0425661P.  
 PR 10-JUN-2003; 2003US-0477453P.  
 PA (RUTP ) UNIV RUTGERS STATE NEW JERSEY.  
 XX PI Montelione GT, Krug RM;  
 XX DR 2004-420083/39.

XX Identifying agents useful for treating influenza virus infection  
 XX PT comprises identifying compounds that inhibit binding between influenza  
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
 PT the protein.  
 XX Disclosure; Page 12; 92PP; English.  
 XX

This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in host cell causes double-stranded-RNA -activated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor eIF2alpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related to the method of the invention.

Sequence 230 AA;

Query Match 92.1%; Score 1079; DB 8; Length 230;

Best Local Similarity 91.7%; Pred. No. 8e-112; Matches 211; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOYDCFLWHRVKRVAQDQBLGDAFLDRLRDKSLLRGGSTLGLNITETAIRA 60  
Db 1 MDSNTVSSFOYDCFLWHRVKRVAQDQBLGDAFLDRLRDKSLLRGGSTLGLNITETAIRA 60

Qy 61 GKQIVERILKESEDEALKNTMASAPASRYLTDMTEEMSRDWFLMLPKVAGPLCIRMD 120  
Db 61 GKQIVERILKESEDEALKNTMASAPASRYLTDMTEEMSRDWFLMLPKVAGPLCIRMD 120

Qy 121 QAIMDKS1LKANF5V1FDRLETLILLRATTEGAIVGELSPSLPGITNEIDKNAIGV 180  
Db 121 QAIMDKN1LKANF5V1FDRLETLILLRATTEGAIVGELSPSLPGITNEIDKNAIGV 180

Qy 181 LIGGLEWNNDTVR5KSTLQRFAWRSSNENGRPLTPKOKRMARTIRESEV 230  
Db 181 LIGGLEWNNDTVR5KSTLQRFAWRSSNEDGRPPBPQKRMARTIRESEV 230

RESULT 4  
AD014178 standard; protein; 217 AA.

AC AD014178;  
XX DT 12-AUG-2004 (first entry)

DB Influenza A virus non-structural protein (NS)-1 #8.

XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
KW double-stranded RNA; dsRNA; binding domain; virucide;  
KW double-stranded-RNA-activated protein kinase; phosphorylation;  
KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.

XX Influenza A virus.

XX WO2004043404-A2.

XX 13 - NOV - 2003 ; 2003WO-US0316292.

XX 13 - NOV - 2002 ; 2002US-0425661P.

PR 10 - JUN - 2003 ; 2003US-0477453P.

XX PA (RUTG ) UNIV RUTGERS STATE NEW JERSEY.

XX PI Montelione GT, Krug RM;

XX 23 - JUN - 2000 ; 2000US-0213650P.

WPI; 2004-420083/39.

XX PT Identifying agents useful for treating influenza virus infection  
PT comprises identifying compounds that inhibit binding between influenza  
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
PT the protein.

XX Disclosure; Page 13; 92PP; English.

This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA -activated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor eIF2alpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related to the method of the invention.

XX SQ Sequence 217 AA;

Query Match 92.0%; Score 1078; DB 8; Length 217;  
Best Local Similarity 96.3%; Pred. No. 9.5e-112; Matches 209; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOYDCFLWHRVKRVAQDQBLGDAFLDRLRDKSLLRGGSTLGLNITETAIRA 60  
Db 1 MDPNTVSSFOYDCFLWHRVKRVAQDQBLGDAFLDRLRDKSLLRGGSTLGLNITETAIRA 60

Qy 61 GKQIVERILKESEDEALKNTMASAPASRYLTDMTEEMSRDWFLMLPKVAGPLCIRMD 120  
Db 61 GKQIVERILKESEDEALKNTMASAPASRYLTDMTEEMSRDWFLMLPKVAGPLCIRMD 120

Qy 121 QAIMDKS1LKANF5V1FDRLETLILLRATTEGAIVGELSPSLPGITNEIDKNAIGV 180  
Db 121 QAIMDKN1LKANF5V1FDRLETLILLRATTEGAIVGELSPSLPGITNEIDKNAIGV 180

Qy 181 LIGGLEWNNDTVR5KSTLQRFAWRSSNENGRPLTPKOKRMARTIRESEV 230  
Db 181 LIGGLEWNNDTVR5KSTLQRFAWRSSNEDGRPPBPQKRMARTIRESEV 230

RESULT 5  
AD005772 standard; protein; 237 AA.

AC ABB05772;  
XX DT 07-MAY-2002 (first entry)

DB Influenza A/udorn/72 (H3N2) Strain NS1 protein SEQ ID NO:18.

AC ABB05772;  
XX KW Influenza A/udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;

KW Influenza A virus; genome.

XX DT 07-MAY-2002 (first entry)

DB Influenzavirus A.

AC WO200200884-A2.

XX PN WO200200884-A2.

XX PD 03 -JAN -2002.

XX PR 21 -JUN -2001 ; 2001WO-US019826.

XX PR 23 -JUN -2000 ; 2000US-0213650P.

XX (AMCY ) AMERICAN CYANAMID CO .  
 XX  
 XX Galarza JM, Latham TE;  
 PI  
 XX  
 DR WPI: 2002-133923/18.  
 DR N-PSDB: ABA93942.  
 XX  
 PT Polynucleotide encoding complete sequence of influenza A/udorn/72 and  
 PT polypeptide, useful in diagnosis and for generating new influenza A  
 PT variant strains.  
 XX Disclosure: Page 78-79; 103pp; English.  
 PS  
 XX  
 CC The present invention describes an isolated polynucleotide (I) having the  
 complete sequence of the influenza A/udorn/72 (H3N2) strain in positive  
 strand, antigenic message sense. ABA93934 to ABA93944 encode the  
 influenza A/udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774  
 from the present invention. (I) is useful for designing polymerase chain  
 reaction (PCR) primers for use in a PCR assay to detect the presence of  
 the corresponding virus segment in a sample or for designing and  
 selecting peptides for use in an enzyme linked immunosorbant assay to  
 detect the presence of the corresponding protein produced by that segment  
 in a sample, hence is useful in diagnosis and may be modified by mutation  
 to generate new influenza A variant strains. ABA94945 to ABA94949  
 represent influenza A/udorn/72 (H3N2) strain sequencing primers, which  
 are used in an example from the present invention.  
 XX  
 SQ Sequence 237 AA;  
 Query Match 91.7%; Score 1075; DB 5; Length 237;  
 Best Local Similarity 90.4%; Pred. No. 2.3e-11; Indels 0; Gaps 0;  
 Matches 208; Conservative 10; Mismatches 12;  
 CC  
 Qy 1 MDPNTVSSFOVDCPMLWYRKVRAOELQDAFLDRRLDQKSLRGRGSTLGNINETAIRA 60  
 1 MDSNTVSSFOVDCPMLWYRKQVVDQELQDAFLDRRLDQKSLRGRGSTLGNINIEATHV 60  
 Db 61 GQKVERLKESEBALQNTMASAPASRYLTIDTIEENSRDWMLMPQKVAQPLCKRM 120  
 Db 61 GQKVERLKESEBALQNTMASAPASRYLTIDTIEENSRDWMLMPQKVAQPLCKRM 120  
 Qy 121 QAIMDKSIIILKANFSVIFDRLETLILLRATFEGAVGEBISPLSPGHTNDIKAIVG 180  
 Db 121 QAIMDRNIMILKANFSVIFDRLETLILLRATFEGAVGEBISPLSPGHTIDVRAIVG 180  
 Qy 181 LIGGLEWNNTTVRSKTLQRFAWRSNENGRPLTPKQRKWMARTIRSEV 230  
 Db 181 LIGGLEWNNTTVRSKTLQRFAWRSNENGRPLTPKQRKWMARTARSKV 230  
 RESULT 6  
 AD014179  
 ID AD014179 standard; protein; 227 AA.  
 XX  
 AC AD014179;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX Influenza A virus non-structural protein (NS)-1 #9.  
 DB  
 XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
 KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
 KW double-stranded RNA; dsRNA; binding domain; virucide;  
 KW double-stranded-RNA-activated protein kinase; phosphorylation;  
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
 KW viral protein replication; screening method; infection.  
 XX  
 OS Influenza A virus.  
 XX  
 PN WO2004043404-A2.  
 XX  
 PD 27-MAY-2004.  
 XX

PF 13-NOV-2003; 2003WO-US03622.  
 XX  
 PA 13-NOV-2002; 2002US-0425661P.  
 PR 10-JUN-2003; 2003US-0477453P.  
 XX  
 PA (RUTP ) UNIV RUTGERS STATE NEW JERSEY.  
 XX  
 PI Montelione GT, Krug RM;  
 XX  
 DR WPI: 2004-420083/39.  
 XX  
 PT Identifying agents useful for treating influenza virus infection  
 PR comprises identifying compounds that inhibit binding between influenza  
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
 PR the protein.  
 XX  
 PS Disclosure; Page 13; 92pp; English.  
 XX  
 CC This invention relates to a novel method of identifying an inhibitor of  
 CC influenza virus which comprises testing candidate compounds for their  
 CC ability to reduce the extent of binding between influenza virus non-  
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
 CC domain and a dsRNA that binds the protein. The invention may be useful  
 CC for the production of compounds with virucide activity acting as  
 CC inhibitors of binding between influenza virus non-structural protein-1  
 CC (NS1) and double-stranded RNA. It is possible that binding of double-  
 CC stranded RNA by the NS1 protein in host cell causes double-stranded-RNA  
 CC -activated protein kinase to remain in an inactive state so that it does  
 CC not catalyse the phosphorylation of translation inhibition factor  
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
 CC replication. The invention is useful as a (high throughput) screening  
 CC method for identifying compounds having inhibitory activity against  
 CC influenza virus. Compounds identified are useful in treating animals,  
 CC including human infected with influenza virus. The present sequence is  
 CC that of an influenza virus non-structural (NS)-1 protein which is related  
 CC to the method of the invention.  
 XX  
 Sequence 227 AA;  
 Query Match 90.2%; Score 1057; DB 8; Length 227;  
 Best Local Similarity 90.7%; Pred. No. 2.3e-109;  
 Matches 206; Conservative 11; Mismatches 10; Indels 0; Gaps 0;  
 CC  
 Qy 4 NTYSSFOVDCPMLWYRKVRAOELQDAFLDRRLDQKSLRGRGSTLGNINETAIRA 63  
 Db 1 NTYSSFOVDCPMLWYRKVRAOELQDAFLDRRLDQKSLRGRGSTLGNINETAIRA 60  
 Qy 64 IVERILKESEBALQNTMASAPASRYLTIDTIEENSRDWMLMPQKVAQPLCKRM 123  
 Db 61 IVERILKESEBALQNTMASAPASRYLTIDTIEENSRDWMLMPQKVAQPLCKRM 120  
 Qy 124 MDKSIILKANFSVIFDRLETLILLRATFEGAVGEBISPLSPGHTNDIKAIVG 183  
 Db 121 MDKSIILKANFSVIFDRLETLILLRATFEGAVGEBISPLSPGHTNDIKAIVG 180  
 Qy 184 GLEWNNTTVRSKTLQRFAWRSNENGRPLTPKQRKWMARTIRSEV 230  
 Db 181 GLEWNNTTVRSKTLQRFAWRSNENGRPLTPKQRKWMARTIRSEV 227  
 RESULT 7  
 AAW03522  
 ID AAW03522 standard; protein; 230 AA.  
 XX  
 AC AAW03522;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 09-APR-1997 (first entry)  
 XX  
 DE Non-structural protein NS1 of influenza A virus.  
 XX  
 KW Non-structural protein; NS1; influenza virus; respiratory tract;  
 KW diagnosis; anti-NS1 antibody; primer; PCR; detection; amplify.

XX Influenza virus; A/equine 1/Suffolk 89.  
 OS PR 16-FEB-2000; 2000US-00506286.  
 XX (UYPI-) UNIV PITTSBURGH.  
 XX PA  
 XX PI Dowling PW, Youngner JS;  
 XX DR WPI; 2001-522584/57.  
 XX DR N-PSDB; AAD15678.  
 XX PR Novel isolated equine influenza virus (wild-type and cold-adapted)  
 PR proteins and viruses containing nucleic acid molecules encoding the  
 PR virus, which are useful for protecting animals from influenza virus  
 PR infections.  
 XX  
 PI Binns M, Birch-Machin I;  
 XX PS Claim 5; Page 72-73; 172pp; English.  
 XX DR The patent discloses cold-adapted equine influenza viruses and  
 XX reassortant influenza A viruses comprising at least one genome segment of  
 XX such an equine influenza virus, wherein the equine influenza genome  
 XX segment confers at least one identifying phenotype of the cold-adapted  
 XX equine influenza virus, such as cold adaptation, temperature sensitivity,  
 XX dominant interference or attenuation. The viruses are useful for  
 XX protecting animals from diseases caused by influenza viruses. They are  
 XX also used as vaccines. The present sequence is an equine influenza (ei)  
 XX virus H3N8 Peiwt (wild type) NS230 protein which is encoded by  
 XX neiwtINS891 DNA  
 SQ Sequence 230 AA;

Query Match	Score 1052;	DB 4;	Length 230;
Best Local Similarity	89.8%;	Pred. No. 8.4e-109;	
Matches 202;	Conservative	16;	Mismatches 12;
Indels 0;	Gaps 0;		

QY 1 MDENTVSSQVQDCPFLWHRKVRQDQELGAPDAPLDLRRDQKSLRGRGSGTIGNIETAIRA 60  
 DB 1 MDSNTVSSQVQDCPFLWHRKVRQDQELGAPDAPLDLRRDQKSLRGRGSGTIGDIETATRA 60  
 QY 61 GKOIVERILKERSDEALKMTMASAPASRYLTDTKMTIERSRDWFLMPKQVKTGTSCLCIRMD 120  
 DB 61 GKOIVLEERILKERSDEALKMTIASPASRYLTDTKMTIERSRDWFLMPKQVKTGTSCLCIRMD 120  
 QY 121 QAIMDKSILKANFSVIFDRLETLILLRAFTEGAIVGEISPLSPLSPHTNEDIKNAIGV 180  
 DB 121 QAIMDKSILKANFSVIFDRLETLILLRAFTEGAIVGEISPLSPLSPHTNEDIKNAIGV 180  
 QY 181 LIGGLEMMNTTIVRSKTLQRFAWRSNSHENGRRPLTPKQKRMARTISBV 230  
 DB 181 LIGGLEMMNTTIVRSKTLQRFAWRSNSHENGRRPLTPKQKRMARTISBV 230  
 RESULT 9  
 AAE09029 standard; protein; 230 AA.  
 XX AAE09029;  
 XX AC  
 XX DT 15-NOV-2001 (first entry)  
 XX DE Equine influenza virus H3N8 PeicalNS230 protein.  
 XX KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;  
 XX KW vaccine; neiwtINS891 DNA; PeicalNS230 protein.  
 XX OS Equine influenza virus H3N8.  
 XX PN WO200160849-A2.  
 XX PD 23-AUG-2001.  
 XX PF 16-FEB-2001; 2001WO-US005048.  
 XX OS WO200160849-A2.  
 XX PD 23-AUG-2001.  
 XX PF 16-FEB-2000; 2000US-00506286.

PR 10-JUN-2003; 2003US-047745P.  
 XX  
 PA (RUTGERS STATE NEW JERSEY.  
 XX  
 PR Montelione GT, Krug RM;  
 XX  
 PR WPI; 2004-420083/39.  
 XX  
 PR Novel agents useful for treating influenza virus infection  
 PR comprises identifying compounds that inhibit binding between influenza  
 PR virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
 PR the protein.  
 XX  
 Disclosure; Page 13; 92pp; English.  
 XX  
 This invention relates to a novel method of identifying an inhibitor of  
 influenza virus which comprises testing candidate compounds for their  
 ability to reduce the extent of binding between influenza virus non-  
 structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
 domain and a dsRNA that binds the protein. The invention may be useful  
 for the production of compounds with a virucide activity acting as  
 inhibitors of binding between influenza virus non-structural protein-1  
 (NS1) and double-stranded RNA. It is possible that binding of double-  
 stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
 -activated protein kinase to remain in an inactive state so that it does  
 not catalyse the phosphorylation of translation inhibition factor  
 eIF2alpha which would otherwise inhibit viral protein synthesis and  
 replication. The invention is useful as a (high throughput) screening  
 method for identifying compounds having inhibitory activity against  
 influenza virus. Compounds identified are useful in treating animals,  
 including human infected with influenza virus. The present sequence is  
 related to that of an influenza virus non-structural (NS)-1 protein which is related  
 to the method of the invention.  
 XX  
 Sequence 227 AA;  
 Query Match 89.8%; Score 1052; DB 4; Length 230;  
 Best Local Similarity 87.8%; Pred. No. 8.4e-109; Mismatches 16; Indels 0; Gaps 0;  
 Matches 202; Conservative 16; Mismatches 11; Indels 0; Gaps 0;  
 YY 1 MDPNTVSSFOVQFCFLWHVRKRAVQDPLRDRQSLRGRTSLGNIETAIRA 60  
 YY 1 MDSNTVSSFOVQFCFLWHVRKRAVQDPLRDRQSLRGRTSLGNIETAIRA 60  
 b 1 MDPNTVSSFOVQFCFLWHVRKRAVQDPLRDRQSLRGRTSLGNIETAIRA 60  
 b 1 MDSNTVSSFOVQFCFLWHVRKRAVQDPLRDRQSLRGRTSLGNIETAIRA 60  
 YY 61 GKVQVERBILKEESDEALKMTMASAPASRYLTIDMTIEEMSRDPMFLMPKQVAGPLCIRMD 120  
 YY 61 GKVQVERBILKEESDEALKMTMASAPASRYLTIDMTIEEMSRDPMFLMPKQVAGPLCIRMD 120  
 b 121 QAIMDKSFLILKANFSVLFDRLETLILRAFFTREGAVGEISLPSLIGHTNEDIKRAGV 180  
 b 121 QAIMDKSFLILKANFSVLFDRLETLILRAFFTREGAVGEISLPSLIGHTNEDIKRAGV 180  
 YY 181 LIGGLENNNTTVRSKTLQRFAWRSSNENGRLPPLTPKOKRKRMTARIEV 230  
 YY 181 LIGGLENNNTTVRSKTLQRFAWRSSNENGRLPPLTPKOKRKRMTARIEV 230  
 b 181 LIGGLKNDNTNTRISETLQRFAWRSSHENGRLPPLTPKOKRKRMTIEPEV 230  
 YY 124 MDKSLILKANFSVLFDRLETLILRAFFTREGAVGEISLPSLIGHTNEDIKRAGV 183  
 YY 124 MDKSLILKANFSVLFDRLETLILRAFFTREGAVGEISLPSLIGHTNEDIKRAGV 183  
 D ADO14177 standard; protein; 227 AA.  
 D ADO14177;  
 D 12-AUG-2004 (first entry)  
 YY Influenza A virus non-structural protein (NS)-1 #7.  
 YY RESULT 10  
 YY D ADO14177  
 YY D ADO14177 standard; protein; 230 AA.  
 YY D ADO14177;  
 YY D 12-AUG-2004 (first entry)  
 YY Influenza A virus non-structural protein (NS)-1 #7.  
 YY influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
 YY double-stranded-RNA; dsRNA; binding domain; virucide;  
 YY double-stranded-RNA-activated protein kinase; phosphorylation;  
 YY translation inhibition factor; eIF2alpha; viral protein synthesis;  
 YY viral protein replication; screening method; infection.  
 YY Influenza A virus.  
 XX WO2004043404-A2.  
 XX 27-MAY-2004.  
 XX 13-NOV-2003; 2003WO-US036292.  
 XX 13-NOV-2003; 2003US-0425661B.  
 XX  
 RESULT 11  
 XX ADO14174  
 XX ID ADO14174 standard; protein; 230 AA.  
 XX  
 AC ADO14174;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 XX Influenza A virus non-structural protein (NS)-1 #4.  
 XX  
 XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
 XX double-stranded-RNA; dsRNA; binding domain; virucide;  
 XX double-stranded-RNA-activated protein kinase; phosphorylation;  
 XX translation inhibition factor; eIF2alpha; viral protein synthesis;  
 XX viral protein replication; screening method; infection.  
 XX





Best Local Similarity 85.7%; Pred. No. 2.5e-10; Mismatches 16; Indels 0; Gaps 0; Matches 197; Conservative 16; Mismatches 17; Indels 0; Gaps 0; CC method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related to the method of the invention.

Qy 1 MDPNTVSSFOVDCFLWHRKRAVDEBLGDAFLDLRDKLGRGSGLGNLTETAIRA 60  
Db 1 MDSNTVSSFOVDCFLWHRKRAVDEBLGDAFLDLRDKLGRGSGLGNLTETAIRA 60  
Qy 61 GKOIVERILKEEDEALKNTMASAPASRYLTDMTEEMSRDWFLMLPKOKVAGPLCIRMD 120  
Db 61 GRHIVRILLEEDEALKNTMASAPASRYLTDMTEEMSRDWFLMLPKOKVAGPLCIRMD 120  
Qy 121 QAIMDKSIIILKANFSVIFDRLTLLIRATFTEGAVIGRISPLSPLGHTNEDIKNAIGV 180  
Db 121 QAVNGKTIILKANFSVIFDRLTLLIRATFTEGAVIGRISPLSPLGHTNEDIKNAIGV 180  
Qy 181 LIGGLEWNNDNTVRVSKTLQPKRPAWSNNGRPPLPKQKRMARTIRSEV 230  
Db 181 LIGGLEWNNDNTVRVSETLQRFTWSSDENGSPSPPKQKRMKVERTIEPEV 230  
RESULT 15  
DB ADO141B4  
ID ADO141B4 standard; protein; 202 AA.  
XX  
AC ADO141B4;  
XX DT 12-AUG-2004 (first entry)  
XX DB Influenza A virus non-structural protein (NS)-1 #14.  
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
KW double-stranded RNA; dsDNA; binding domain; virucide;  
KW double-stranded-RNA-activated protein kinase; phosphorylation;  
KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.  
XX OS Influenza A virus; STRAIN A/FORT MONMOUTH/1/47.  
PN WO200403404-A2.  
XX PD 27-MAY-2004.  
XX PF 13-NOV-2003; 2003WO-US036292.  
XX PR 13-NOV-2002; 2002US-0425661P.  
PR 10-JUN-2003; 2003US-047453P.  
XX PA (RUTTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX PI Montelione GT, Krug RM;  
XX DR WPI: 2004-420083/39.  
XX PT Identifying agents useful for treating influenza virus infection  
PT comprises identifying compounds that inhibit binding between influenza  
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
PT the protein.  
XX PS Disclosure; Page 14; 92pp; English.  
XX This invention relates to a novel method of identifying an inhibitor of  
CC influenza virus which comprises testing candidate compounds for their  
CC ability to reduce the extent of binding between influenza virus non-  
structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
CC domain and a dsRNA that binds the protein. The invention may be useful  
CC for the production of compounds with a virucide activity acting as  
CC inhibitors of binding between influenza virus non-structural protein-1  
CC (NS1) and double-stranded RNA. It is possible that binding of double-  
stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
CC -activated protein kinase to remain in an inactive state so that it does  
CC not catalyse the phosphorylation of translation inhibition factor  
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
CC replication. The invention is useful as a (high throughput) screening

Query Match 85.8%; Score 1006; DB 8; Length 202;  
Best Local Similarity 97.5%; Pred. No. 9.8e-10; Mismatches 3; Indels 0; Gaps 0;  
Matches 197; Conservative 197; Score 1006; DB 8; Length 202;  
Qy 1 MDPNTVSSFOVDCFLWHRKRAVDEBLGDAFLDLRDKLGRGSGLGNLTETAIRA 60  
Db 1 MDPNTVSSFOVDCFLWHRKRAVDEBLGDAFLDLRDKLGRGSGLGNLTETAIRA 60  
Qy 61 GKOIVERILKEEDEALKNTMASAPASRYLTDMTEEMSRDWFLMLPKOKVAGPLCIRMD 120  
Db 61 GKOIVERILKEEDEALKNTMASAPASRYLTDMTEEMSRDWFLMLPKOKVAGPLCIRMD 120  
Qy 121 QAIMDKSIIILKANFSVIFDRLTLLIRATFTEGAVIGRISPLSPLGHTNEDIKNAIGV 180  
Db 121 QAMDKSIIILKANFSVIFDRLTLLIRATFTEGAVIGRISPLSPLGHTNEDIKNAIGV 180  
Qy 181 LIGGLEWNNDNTVRVSKTLQPKRPAWSNNGRPPLPKQKRMARTIRSEV 230  
Db 181 LIGGLEWNNDNTVRVSETLQRFTWSSDENGSPSPPKQKRMKVERTIEPEV 230  
Qy 121 QAMDKSIIILKANFSVIFDRLTLLIRATFTEGAVIGRISPLSPLGHTNEDIKNAIGV 180  
Db 121 QAMDKSIIILKANFSVIFDRLTLLIRATFTEGAVIGRISPLSPLGHTNEDIKNAIGV 180  
Qy 181 LIGGLEWNNDNTVRVSKTLQKFA 202  
Db 181 LIGGLEWNNDNTVRVSKTLQKFA 202

Search completed: September 22, 2005, 21:42:21  
Job time : 159.61 secs

GenCore version 5.1.6  
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## OM protein - protein search, using Bw model

Run on: September 22, 2005, 21:33:28 ; Search time 32.1083 Seconds

(without alignments)  
 689.226 Million cell updates/sec

Title: US-10-654-737-5

Perfect score: 1172

Sequence: 1 MDENTVSSFQVDCFLWVRK. .... .RPPLTPQKRK MARTIRSEV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79;\*

1: piri;\*

2: pir2;\*

3: pir3;\*

4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1142	97.4	237	1 MNIV77	nonstructural prot
2	9	97.3	237	1 MNIV14	nonstructural prot
3	1128	96.2	237	1 MNIVC1	nonstructural prot
4	1111	94.8	230	1 MNIV1	nonstructural prot
5	1107	94.5	230	2 MN9648	nonstructural prot
6	1092	93.2	230	1 MNIV2	nonstructural prot
7	1079	92.1	230	1 MNIV3	nonstructural prot
8	1078	92.0	217	1 MNIV61	nonstructural prot
9	1075	91.7	230	1 MNIV4	nonstructural prot
10	1075	91.7	237	1 MNIV1A	nonstructural prot
11	1061	90.5	227	1 MNIVX3	nonstructural prot
12	1057	90.2	227	1 MNIVX9	nonstructural prot
13	1057	90.2	230	1 MNIV1P	nonstructural prot
14	1055	90.0	230	1 MNIV1	nonstructural prot
15	1050	89.6	227	1 MNIVX5	nonstructural prot
16	1050	89.6	237	1 MNIV1K	nonstructural prot
17	1049	89.5	227	1 MNIVX7	nonstructural prot
18	1046	89.2	227	1 MNIVX1	nonstructural prot
19	1029	87.8	230	1 D5539	nonstructural prot
20	999	85.2	202	1 MNIV47	nonstructural prot
21	844	72.0	230	1 MNIV16	nonstructural prot
22	840	71.7	230	1 MNIVAS	nonstructural prot
23	840	71.7	230	1 MNIVA6	nonstructural prot
24	838	71.5	230	1 MNIVAB	nonstructural prot
25	837	71.4	230	1 MNIV7	nonstructural prot
26	824	70.3	230	2 AS5575	nonstructural prot
27	437	37.3	89	2 B22982	nonstructural prot
28	411	35.1	124	1 MNIV71	nonstructural prot
29	12.9	32	2 P0419	nonstructural prot	

## ALIGNMENTS

RESULT 1							
MNIV77							
C;Species: influenza A virus							
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 16-Jul-1999							
C;Accession: E92991; A04090							
R;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.							
J;Virol. 45, 547-554, 1983							
A;Title: Sequential mutations in the NS genes of influenza virus field strains.							
A;Reference number: A92991; MUID: 83164298; PMID: 6834466							
A;Accession: E92991							
A;Molecule type: genomic RNA							
A;Residues: 1-237 <KR>							
A;Cross-references: GB:K00578; PIDN:AAA3540.1; PMID:9324841							
C;Genetics:							
A;Map position: segment 8							
C;Superfamily: influenza virus nonstructural protein NS1							
C;Keywords: alternative splicing							
Query Match	97.4%	Score	1142;	DB 1;	Length	237;	
Best Local Similarity	97.0%	Pred. No.	3.1e-91;				
Matches 223;	Conservative	4;	Mismatches 3;	Indels 0;	Gaps 0;		

  

RESULT 2							
MNIV14							
C;Species: influenza A virus							
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999							
C;Accession: A92991; A04090; B92982							
R;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.							
J;Virol. 45, 547-554, 1983							
A;Title: Sequential mutations in the NS genes of influenza virus field strains.							
A;Reference number: A92991; MUID: 83164298; PMID: 6834466							
A;Accession: A92991							
A;Molecule type: genomic RNA							

A;Residues: 1-237 <KRY>  
 A;Cross-references: GB:K00576; NID:9324813; PID:9324815  
 C;Genetics:  
 A;Map position: segment 8  
 C;Superfamily: influenza virus nonstructural protein NS1  
 C;Keywords: alternative splicing

Query Match 97.3%; Score 1140; DB 1; Length 237;  
 Best Local Similarity 96.3%; Pred. No. 4.6e-91;  
 Matches 222; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 1 MDPTVSSFQVDCFLWHRKRVADQELGDAFLDRDOKSLRGRGSLTGLNIEETAIRA 60  
 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120  
 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120

Qy 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180  
 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180

Db 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180  
 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180

Qy 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230  
 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230

Db 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230  
 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230

RESULT 3  
 MN1VCL  
 nonstructural protein NS1 - influenza A virus (strain A/Chile/1/83 [H1N1])  
 C;Species: influenza A virus  
 C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text\_change 07-Jun-1996  
 C;Accession: A34215; S04836  
 R;Schreier, E.;Roeske, H.; Michel, S.  
 Nucleic Acids Res. 17, 5381, 1989  
 A;Title: Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83 (H1N1).  
 A;Reference number: A34215; PMID:89345097; PMID:2762132  
 A;Accession: A34215  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-237 <SCH>  
 A;Cross-references: EMBL:X15282  
 C;Genetics:  
 A;Map position: segment 8  
 C;Superfamily: influenza virus nonstructural protein NS1  
 C;Keywords: alternative splicing; nonstructural protein

Query Match 96.2%; Score 1126; DB 1; Length 237;  
 Best Local Similarity 95.2%; Pred. No. 5e-90; Mismatches 7; Indels 4; Gaps 0;

Db 1 MDPTVSSFQVDCFLWHRKRVADQELGDAFLDRDOKSLRGRGSLTGLNIEETAIRA 60  
 1 MDPTVSSFQVDCFLWHRKRVADQELGDAFLDRDOKSLRGRGSLTGLNIEETAIRA 60

Qy 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120  
 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120

Db 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180  
 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180

Qy 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230  
 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230

Db 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230  
 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230

RESULT 4  
 MN1V1  
 nonstructural protein NS1 - influenza A virus (strain A/PR/8/34)

C;Date: 30-Apr-1981 #sequence\_revision 30-Apr-1981 #text\_change 30-Sep-1993  
 C;Accession: A04089  
 R;Biez, M.; Taussig, R.; Zazra, J.J.; Young, J.P.; Palese, P.; Reisfeld, A.; Skalka, A.M.  
 Nucleic Acids Res. 8, 5845-5858, 1980  
 A;Title: Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and comparison  
 A;Reference number: A93714; MUID:81124304; PMID:7465426  
 A;Accession: A04089  
 A;Molecule type: Genomic RNA  
 A;Residues: 1-230 <BAE>  
 C;Genetics:  
 A;Map position: segment 8  
 C;Superfamily: influenza virus nonstructural protein NS1  
 C;Keywords: alternative splicing  
 Query Match 94.8%; Score 1111; DB 1; Length 230;  
 Best Local Similarity 93.9%; Pred. No. 1.e-88;  
 Matches 216; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Db 1 MDPTVSSFQVDCFLWHRKRVADQELGDAFLDRDOKSLRGRGSLTGLNIEETAIRA 60  
 1 MDPTVSSFQVDCFLWHRKRVADQELGDAFLDRDOKSLRGRGSLTGLNIEETAIRA 60

Qy 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120  
 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120

Db 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120  
 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120

Qy 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180  
 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180

Db 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180  
 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180

Qy 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230  
 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230

Db 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230  
 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230

RESULT 5  
 S09648  
 nonstructural protein NS1 - influenza A virus (strain A/Leningrad/1/54)  
 C;Species: influenza A virus  
 C;Accession: S09648  
 C;Date: 21-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 19-May-2000  
 C;Cross-references: EMBL:X52146; NID:960716; PID:CAA36392.1; PID:g60717  
 R;Beklemishay, A.B.; Blinov, V.M.; Vassilenko, S.K.; Karginov, V.A.; Mamat  
 Biaoq. Khim. 11, 641-645, 1985  
 A;Title: Synthesis, cloning and sequencing of a full-length DNA copy of the fragment 8 of  
 A;Reference number: S09648; MUID:85307107; PMID:403350  
 A;Accession: S09648  
 A;Status: preliminary; translation not shown  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:X52146; NID:960716; PID:CAA36392.1; PID:g60717  
 C;Superfamily: influenza virus nonstructural protein NS1  
 C;Keywords: translation not shown

Query Match 94.5%; Score 1107; DB 2; Length 230;  
 Best Local Similarity 93.5%; Pred. No. 3.1e-88;  
 Matches 215; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Db 1 MDPTVSSFQVDCFLWHRKRVADQELGDAFLDRDOKSLRGRGSLTGLNIEETAIRA 60  
 1 MDPTVSSFQVDCFLWHRKRVADQELGDAFLDRDOKSLRGRGSLTGLNIEETAIRA 60

Qy 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120  
 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120

Db 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120  
 61 GQIIVERILKEESDEALKTMVASAPASRYLTDMTEEMSDWFMLMPKQKVAGPLCIRMD 120

Qy 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180  
 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180

Db 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180  
 121 QAIMDKSIIKANFSVIFDRLETLILLRAFFEEGAIVGEISPLSPLGHTNEDIKNAIGV 180

Qy 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230  
 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230

Db 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230  
 181 LIGGLEWNNTNTRVSKTLQRFAWRSNNENGRPLTPKQKRMARTIRSEV 230



Qy	1	MDPNTVSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRA	60	C;Accession: C27846 R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S. Virology 158, 465-468, 1987
Db	1	MDSNVSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRA	60	A;Title: Genetic divergence of the NS genes of avian influenza viruses. A;Reference number: A94361; MUID:87236215; PMID:2954302
Qy	61	GKQIVERILKEESEDEALKMTMASAPASRYLTDMTLEEMSRDWFLMPKVKAGPLCIRMD	120	A;Accession: C27846 A;Molecule type: genomic RNA
Db	61	GKQIVERILKEESEDEALKMTMASAPASRYLTDMTLEEMSRDWFLMPKVKAGPLCIRMD	120	A;Residues: 1-227 <NAK> A;Cross-references: GB:MI6563; NID:9324786; PMID:AAA43510-1; PID:9324787
Qy	121	QAIMDKSIIILKANPSVIFDRLTLLRAFTEEGAVGTSPLPSLPGHTNEDIKNAIGV	180	A;Gene: NS1 A;Map position: segment 8 C;Superfamily: influenza virus nonstructural protein NS1 C;Keywords: alternative splicing; nonstructural protein
Db	121	QAIMDKSIIILKANPSVIFDRLTLLRAFTEEGAVGTSPLPSLPGHTNEDIKNAIGV	180	C;Genetics:
Qy	181	LIGGLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV	230	Query Match 90.5%; Score 1061; DB 1; Length 227; Best Local Similarity 91.2%; Pred. No. 2, 9e-84; Indels 0; Gaps 0; Matches 207; Conservative 11; Mismatches 9;
Db	181	LIGGLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV	230	Qy 4 NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 63 Db 1 NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 60
Qy	181	LIGGLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV	230	64 IVERILKEESEDEALKMTMASAPASRYLTDMTLEEMSRDWFLMPKVKAGPLCIRMDQAI 123 Db 61 IVERILKEESEDEALKMTMASAPASRYLTDMTLEEMSRDWFLMPKVKAGPLCIRMDQAI 120
Qy	181	LIGGLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV	230	124 MDKSLILKANPSVIFDRLTLLRAFTEEGAVGTSPLPSLPGHTNEDIKNAIGVIG 183 Db 121 MDKSLILKANPSVIFDRLTLLRAFTEEGAVGTSPLPSLPGHTNEDIKNAIGVIG 180
Db	181	LIGGLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV	230	184 GLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV 230 Db 181 GLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV 227
RESULT 1.2				
Qy	1	MNIVX9 nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1])	63	MNIVX9 nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fragment) C;Species: influenza A virus C;Date: 31-Oct-1980 #text_change 31-Oct-1980 #text_change 09-Jul-2004
Db	1	NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 63	64 IVERILKEESEDEALKMTMASAPASRYLTDMTLEEMSRDWFLMPKVKAGPLCIRMDQAI 123	
Qy	1	NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 60	61 IVERILKEESEDEALKMTMASAPASRYLTDMTLEEMSRDWFLMPKVKAGPLCIRMDQAI 120	
Db	1	NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 60	124 MDKSLILKANPSVIFDRLTLLRAFTEEGAVGTSPLPSLPGHTNEDIKNAIGVIG 183 Db 121 MDKSLILKANPSVIFDRLTLLRAFTEEGAVGTSPLPSLPGHTNEDIKNAIGVIG 180	
Qy	1	NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 63	184 GLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV 230 Db 181 GLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV 227	
RESULT 1.2				
Qy	1	MNIVX9 nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1])	63	MNIVX9 nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fragment) C;Species: influenza A virus C;Date: 30-Feb-1989 #text_change 30-Sep-1989 #text_change 16-Jul-1999
Db	1	NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 63	64 IVERILKEESEDEALKMTMASAPASRYLTDMTLEEMSRDWFLMPKVKAGPLCIRMDQAI 123 Db 1 NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 60	
Qy	1	NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 60	61 IVERILKEESEDEALKMTMASAPASRYLTDMTLEEMSRDWFLMPKVKAGPLCIRMDQAI 120	
Db	1	NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 60	124 MDKSLILKANPSVIFDRLTLLRAFTEEGAVGTSPLPSLPGHTNEDIKNAIGVIG 183 Db 121 MDKSLILKANPSVIFDRLTLLRAFTEEGAVGTSPLPSLPGHTNEDIKNAIGVIG 180	
Qy	1	NTYSSFOVDCFLWHVRKRAVQDGLDAPFLDLRDKSLSURGRGSLTGNIETAIRAGKQ 63	184 GLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV 230 Db 181 GLEWNNTVSKTLQRFAWSSNENGRPLTPKQRKMMARTIRSEV 227	
RESULT 11				
Qy	1	MNIVX9 nonstructural protein NS1 - influenza A virus (strain A/Duck/England/56 [H1N6])	63	MNIVX9 nonstructural protein NS1 - influenza A virus (strain A/Duck/England/56 [H1N6]) (fragment) C;Species: influenza A virus C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

Db	181	GLENDNTVSETLQRFAVSSNEDGRPPPKQKRMARTIESEV	227	QATMDKSIILKANPSVIFDRLTILLRAFTEEGAIIGEISPLPSLPGHTNEDIKNAIGV	180
<b>RESULT 13</b>					
MNIV1_F		nonstructural protein NS1 - influenza A virus		QATMDKSIILKANPSVIFDRLTILLRAFTEEGAIIGEISPLPSLPGHTNEDIKNAIGV	180
C;Species: influenza A virus				Db	181 QATMDKSIILKANPSVIFDRLTILLRAFTEEGAIIGEISPLPSLPGHTNEDIKNAIGV
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 30-Sep-1993					
C;Accession: A4091					
R;Porter, A.G.; Smith, J.C.; Emtage, J.S.					
Proc. Natl. Acad. Sci. U.S.A. 77, 5074-5078, 1980					
A;Title: Nucleotide sequence of influenza virus RNA segment 8 indicates that coding regi					
A;Reference number: A93838; MUID:81054909; PMID:6254054					
A;Accession: A4091					
A;Molecule type: mRNA					
A;Residues: 1-230 <POR>					
A;Experimental source: strain Rostock					
C;Superfamily: influenza virus nonstructural protein NS1					
C;Keywords: alternative splicing					
Query Match 90.2%; Score 1057; DB 1; Length 230;					
Best Local Similarity 88.3%; Pred. No. 6.6e-84;					
Matches 203; Conservative 16; Mismatches 11; Indels 0; Gaps 0;					
Db	1	MDPNTVSSFOVDCFLWHRKRAVADQELGDAFLDRDQSLRGRGSTLGNLTETAIRA	60	MINIV5	
Db	1	MDSNTVSSFOVDCFLWHRKRAVADQELGDAFLDRDQSLRGRGSTLGNLTETAIRV	60	C;Species: influenza A virus	
Qy	61	GKQIVERILKEESDEALKMTMASAPASRYLTDMTLEEMMSRDWFLMLPKQKAVAGPLCIRMD	120	C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999	
Db	61	GKQIVERILKEESDEALKMTMASAPASRYLTDMTLEEMMSRDWFLMLPKQKAVAGSLCIRMD	120	C;Accession: E27846	
Qy	121	QATMDKSIILKANPSVIFDRLTILLRAFTEEGAIIGEISPLPSLPGHTNEDIKNAIGV	180	C;Cross-references: GB:MI6564; PID:9324875; PID:9324872-1; PID:9324876	
Db	121	QATMDKSIILKANPSVIFDRLTILLRAFTEEGAIIGEISPLPSLPGHTNEDIKNAIGV	180	C;Keywords: alternative splicing; nonstructural protein	
Qy	181	LIGGLEWNNTVRSKTLQRFAVSSNENGRLPQKQKRMARTIESEV	230	C;Genetics: NS1	
Db	181	LIGGLEWNNTVRSKTLQRFAVSSNENGRLPQKQKRMARTIESEV	230	A;Map position: segment 8	
Query Match 89.6%; Score 1050; DB 1; Length 227;				A;Residues: 1-227 <NAK>	
Best Local Similarity 91.2%; Pred. No. 2.6e-83;				A;Cross-references: GB:MI6564; PID:9324875; PID:9324872-1; PID:9324876	
Matches 207; Conservative 9; Mismatches 11; Indels 0; Gaps 0;				A;Gene: NS1	
Db	64	IVERILKEESDEALKMTMASAPASRYLTDMTLEEMMSRDWFLMLPKQKAVAGPLCIRMD	123	A;Map position: influenza virus nonstructural protein NS1	
Qy	64	IVERILKEESDEALKMTMASAPASRYLTDMTLEEMMSRDWFLMLPKQKAVAGSLCIRMD	123	C;Superfamily: influenza virus nonstructural protein	
Db	61	IVERILKEESDEALKMTMASAPASRYLTDMTLEEMMSRDWFLMLPKQKAVAGSLCIRMD	120	C;Keywords: alternative splicing; nonstructural protein	
Qy	124	MDKSIILKANPSVIFDRLTILLRAFTEEGAIIGEISPLPSLPGHTNEDIKNAIGVLIG	183	A;Map position: segment 8	
Db	124	MDKSIILKANPSVIFDRLTILLRAFTEEGAIIGEISPLPSLPGHTNEDIKNAIGVLIG	180	C;Cross-references: GB:MI6564; PID:9324875; PID:9324872-1; PID:9324876	
Query Match 90.0%; Score 1055; DB 1; Length 230;				A;Gene: NS1	
Best Local Similarity 89.6%; Pred. No. 9.8e-84;				C;Superfamily: influenza virus nonstructural protein NS1	
Matches 206; Conservative 13; Mismatches 11; Indels 0; Gaps 0;				C;Keywords: alternative splicing; nonstructural protein	
Db	1	MDPNTVSSFOVDCFLWHRKRAVADQELGDAFLDRDQSLRGRGSTLGNLTETAIRA	60	A;Map position: segment 8	
Qy	1	MDPNTVSSFOVDCFLWHRKRAVADQELGDAFLDRDQSLRGRGSTLGNLTETAIRA	60	C;Cross-references: GB:MI6564; PID:9324875; PID:9324872-1; PID:9324876	
Db	1	MDSNTVSSFOVDCFLWHRKRAVADQELGDAFLDRDQSLRGRGSTLGNLTETAIRV	60	A;Gene: NS1	
Qy	61	GKQIVERILKEESDEALKMTMASAPASRYLTDMTLEEMMSRDWFLMLPKQKAVAGPLCIRMD	120	C;Cross-references: GB:MI6564; PID:9324875; PID:9324872-1; PID:9324876	
Db	61	GKQIVERILKEESDEALKMTMASAPASRYLTDMTLEEMMSRDWFLMLPKQKAVAGSLCIRMD	120	A;Map position: segment 8	

Search completed: September 22, 2005, 21:47:01  
Job time : 34.1083 secs



GN Name=NS; Synonyms=8;  
OS Influenza A virus (strain A/US/90/77 H1N1).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A.  
OC NCBI\_TaxID=225083;  
RN [1]  
SEQUENCE FROM N.A. PubMed=6834468;  
RP MEDLINE=8164298; PubMed=6834468;  
RA Kryszl M., Buonagurio D.A., Young J.P., Palese P.;  
RT "Segmental mutations in the NS genes of influenza virus field  
strains."  
RL J. Virol. 45:547-554 (1983).  
CC - ALTERNATIVE PRODUCTS:  
Event/Alternative splicing; Named isoforms=2;  
Name=NS1;  
ISoD=PO3498-1; Sequence=External;  
ISoD=PO3504-1; Sequence=External;  
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or send an email to license@isb-sib.ch).  
CC  
DR EMBL; K00578; AAA43540.1; -.  
DR HSSP; P03495; INS1.  
DR InterPro; IPR000256; Flu NS1.  
DR InterPro; IPR009068; S157NS1\_bind.  
DR ProDom; PF00613; Flu NS1; 1.  
DR ProDom; PF0600; Flu NS1; 1.  
DR InterPro; IPR009068; S157NS1\_bind.  
KW Alternative splicing; Nonstructural proteins.  
SQ SEQUENCE 237 AA; 26890 MW;  
Query Match 97.4%; Score 1142; DB 1; Length 237;  
Best Local Similarity 97.0%; Pred. No. 1.4e-88;  
Matches 222; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MDPTVSSQVDCPFLWHRKVAQDQLGDAFLDLRDRDQKS1RGRGSTLGLN1ETAIRA 60  
Db 1 GQ1VERILKEESDEALKMTMASAPASRYLTDMT1EEMSDWFLMPKQVAGPLCIRMD 120  
Qy 61 GQ1MDKSTILKANFSVTFDLRFLILLRAFEGAVGEISPLPSLPGHTNEDIKNAIGV 180  
Db 121 GQ1MDKSTILKANFSVTFDLRFLILLRAFEGAVGEISPLPSLPGHTNEDIKNAIGV 180  
Qy 121 GQ1MDKSTILKANFSVTFDLRFLILLRAFEGAVGEISPLPSLPGHTNEDIKNAIGV 180  
Db 121 GQ1MDKSTILKANFSVTFDLRFLILLRAFEGAVGEISPLPSLPGHTNEDIKNAIGV 180  
Qy 181 LIGGLENNNTTVRSKTLQRFPAWSSNNERPRPLTPKOKRMARTIRSEV 230  
Db 181 LIGGLENNNTTVRSKTLQRFPAWSSNNERPRPLTPKOKRMARTIRSEV 230

RESULT 3  
Q6XTT4 PRELIMINARY; PRT; 237 AA.  
ID Q6XTT4.  
AC Q6XTT4.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DB 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
OS Influenza A virus (A/Sao Paulo/3/59 (H2N2)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A; H2N2 subtype.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lindstrom S.E., Cox N.J., Klimov A.;  
OS Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
NCBI\_TaxID=220956;  
RN SEQUENCE FROM N.A.  
RA Lindstrom S.E., Cox N.J., Klimov A.;  
AC Q6XTT6; PRELIMINARY; PRT; 237 AA.  
ID Q6XTT6.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Non-structural protein NS1.  
OS Influenza A virus (A/Victoria/15681/59 (H2N2)).  
OC Influenza virus A; H2N2 subtype.  
NCBI\_TaxID=220956;  
RN SEQUENCE FROM N.A.  
RA Lindstrom S.E., Cox N.J., Klimov A.;  
AC Q6XTT8; PRELIMINARY; PRT; 237 AA.  
ID Q6XTT8.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Non-structural protein NS1.  
OS Influenza A virus (A/Victoria/15681/59 (H2N2)).  
OC Influenza virus A; H2N2 subtype.  
NCBI\_TaxID=220956;  
RN SEQUENCE FROM N.A.  
RA Lindstrom S.E., Cox N.J., Klimov A.;  
OS Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
NCBI\_TaxID=220955;

Query Match 97.4%; Score 1142; DB 2; Length 237;  
Best Local Similarity 96.5%; Pred. No. 1.4e-88;  
Matches 222; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MDPTVSSQVDCPFLWHRKVAQDQLGDAFLDLRDRDQKS1RGRGSTLGLN1ETAIRA 60  
Db 1 MDPTVSSQVDCPFLWHRKVAQDQLGDAFLDLRDRDQKS1RGRGSTLGLN1ETAIRA 60  
Qy 61 GQ1VERILKEESDEALKMTMASAPASRYLTDMT1EEMSDWFLMPKQVAGPLCIRMD 120  
Db 61 GQ1VERILKEESDEALKMTMASAPASRYLTDMT1EEMSDWFLMPKQVAGPLCIRMD 120  
Qy 121 GQ1MDKSTILKANFSVTFDLRFLILLRAFEGAVGEISPLPSLPGHTNEDIKNAIGV 180  
Db 121 GQ1MDKSTILKANFSVTFDLRFLILLRAFEGAVGEISPLPSLPGHTNEDIKNAIGV 180  
Qy 181 LIGGLENNNTTVRSKTLQRFPAWSSNNERPRPLTPKOKRMARTIRSEV 230  
Db 181 LIGGLENNNTTVRSKTLQRFPAWSSNNERPRPLTPKOKRMARTIRSEV 230

Db	181 LIGGLEWNNDNTVRVSCTLQRPAVRSNNENGRPPLTPKQKRMARTIRSKV	230	RESULT 5	PRELIMINARY;	PRT;	237 AA.
			Q6XTJ6	PRELIMINARY;	PRT;	237 AA.
AC	Q6XTJ6		ID	Q6XTJ6	PRT;	237 AA.
DT	05-JUL-2004	(TREMBLrel. 27, Created)				
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)				
DB	Non-structural protein NS1.					
OS	Influenza A virus (A/Davis/1/57(H2N2)).					
OC	ssRNA negative-strand viruses; Orthomyxoviridae;					
OC	Influenza virus A; H2N2 subtype.					
NCBI_TaxID	220951;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Lindstrom S.E., Cox N.J., Klimov A.;					
RL	Submitted (JAN-03) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: AV210153; AAC046571.1;					
HSSP						
DR	InterPro: IPR00256; Flu NS1.					
DR	InterPro: IPR009068; S157NS1_bind.					
DR	Pfam: PF00600; Flu NS1.1.					
DR	ProDom: PD000613; Flu NS1.1.					
DR	InterPro: IPR009068; S157NS1_bind.					
DR	ProDom: PD000613; Flu NS1.1.					
DR	ProDom: PD000613; Flu NS1.1.					
SQ	SEQUENCE 237 AA; 26972 MW; 88D2935CF4409ED6 CRC64;					
Query Match	97.4%;	Score 1142;	DB 2;	Length 237;		
Best Local Similarity	96.5%;	Pred. No. 1.4e-88;				
Matches 222;	Conservative 5;	Mismatches 3;	Indels 0;	Gaps 0;		
Qy	1	MDPNTVSSQVDCPLWHRVKRVAQDLGDAFLDRDOKSLSLGRGSTLGLNLTETAIRA 60				
Db	1	MDPNTVSSQVDCPLWHRVKRVAQDLGDAFLDRDOKSLSLGRGSTLGLNLTETATRV 60				
Qy	61	GKQ1VERILKEEDSDEALKTMASAPASRYLTDMDTBEMSPDWPLMPKOKVAGPLCIRMD 120				
Db	61	GKQ1VERILKEEDSDEALKTMASAPASRYLTDMDTBEMSPDWPLMPKOKVAGPLCIRMD 120				
Qy	121	QAIMDKS1ILKANFSVIFDRLTLLILRAFTEGAAVGETSPLSPLGHTEEDIKNAIGV 180				
Db	121	QAIMDKS1ILKANFSVIFDRLTLLILRAFTEGAAVGETSPLSPLGHTEEDIKNAIGV 180				
Qy	181	LIGGLEWNNDNTVRSKTLQRPAVRSNNENGRPPLTPKQKRMARTIRSKV 230				
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RESULT 6						
VNS1_IAE1	STANDARD;	PRT;	230 AA.			
AC	P26131;					
DT	01-MAY-1992 (Rel. 22, Created)					
DT	01-MAY-1992 (Rel. 22, Last sequence update)					
DT	05-JUL-2004 (Rel. 44, Last annotation update)					
DE	Non-structural protein NS1.					
GN	Name=8;					
OS	Influenza A virus (strain A/Leningrad/134/57 H2N2), and					
OS	Influenza A virus (strain A/Leningrad/134/17/57 H2N2), and					
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;					
OC	Influenza virus A.					
OX	NCBI_TaxID=128148, 152281, 152282;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	SEQUENCE FROM N.A. PubMed=1733114;					
RA	Klimov A.I., Cox N.J., Yotov W.V., Rocha E., Alexandra G.I., Kendal A.P.;					
RA	"Sequence changes in the live attenuated, cold-adapted variants of influenza A/Leningrad/134/57 (H2N2) virus."					
RT	Virology 186: 795-797 (1992).					
RL	ALTERNATIVE PRODUCTS:					

CC	Event=Alternative splicing; Named isoforms=2;					
CC	Name=NS1;					
CC	ISOId=P26131-1; Sequence=Displayed;					
CC	ISOId=P21432-1, P26133-1;					
CC	Sequence=External;					
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CC	EMBL: M81572; AAC19199.1; ALT TERM.					
DR	EMBL: M81578; AAC19201.1; ALT TERM.					
DR	EMBL: M81584; AAC19203.1; ALT TERM.					
DR	HSSP; P0495; NS1.					
DR	InterPro: IPR00256; Flu NS1.					
DR	InterPro: IPR009068; S157NS1_bind.					
DR	Pfam: PF00600; Flu NS1.1.					
DR	ProDom: PD000613; Flu NS1.1.					
KW	Alternative splicing; Nonstructural protein.					
SEQUENCE	230 AA;	2696 MW;	D3B86B15A70CE97 CRC64;			
Query Match	97.4%;	Score 1141;	DB 1;	Length 230;		
Best Local Similarity	96.5%;	Pred. No. 1.7e-88;				
Matches 222;	Conservative 5;	Mismatches 3;	Indels 0;	Gaps 0;		
Qy	1	MDPNTVSSQVDCPLWHRVKRVAQDLGDAFLDRDOKSLSLGRGSTLGLNLTETAIRA 60				
Db	1	MDPNTVSSQVDCPLWHRVKRVAQDLGDAFLDRDOKSLSLGRGSTLGLNLTETATRV 60				
Qy	61	GKQ1VERILKEEDSDEALKTMASAPASRYLTDMDTBEMSPDWPLMPKOKVAGPLCIRMD 120				
Db	61	GKQ1VERILKEEDSDEALKTMASAPASRYLTDMDTBEMSPDWPLMPKOKVAGPLCIRMD 120				
Qy	121	QAIMDKS1ILKANFSVIFDRLTLLILRAFTEGAAVGETSPLSPLGHTEEDIKNAIGV 180				
Db	121	QAIMDKS1ILKANFSVIFDRLTLLILRAFTEGAAVGETSPLSPLGHTEEDIKNAIGV 180				
Qy	181	LIGGLEWNNDNTVRSKTLQRPAVRSNNENGRPPLTPKQKRMARTIRSKV 230				
Db	181	LIGGLEWNNDNTVRSKTLQRPAVRSNNENGRPPLTPKQKRMARTIRSKV 230				
RESULT 7						
Q6XTJ2						
ID	Q6XTJ2					
AC	Q6XTJ2					
DT	05-JUL-2004 (TREMBLrel. 27, Created)					
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)					
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)					
DB	Non-structural protein NS1.					
OS	Influenza A virus (A/B1Salvador/2/57(H2N2)).					
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;					
OC	Influenza virus A; H2N2 subtype.					
NCBI_TaxID	220952;					
RN						
RP	SEQUENCE FROM N.A.					
RA	Lindstrom S.E., Cox N.J., Klimov A.;					
RA	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.					
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: AV210155; AAC046575.1; -.					
DR	HSSP; P03495; IAL1.					
DR	GO:0003723; P:RNA binding; IEA.					
DR	InterPro: IPR009068; S157NS1_bind.					
DR	Pfam: PF00600; Flu NS1; 1.					
DR	ProDom: PD000613; Flu NS1; 1.					
SQ	SEQUENCE 237 AA;	26943 MW;	88D29340BER944C3 CRC64;			
Query Match	97.4%;	Score 1141;	DB 2;	Length 237;		



AC	Q6XTJ8;	Db	1 MDSNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTBTATRV 60
DT	05-JUL-2004 (TREMBLrel. 27, Created)	Qy	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	Db	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DT	05-JUL-2004 (TREMBLrel. 7, Last annotation update)	Qy	121 QAIMDKS11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
DB	Non-structural protein NS1.	Db	121 QAIMDKS11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
OS	Influenza A virus (A/Albany/7/52 (H2N2))	Qy	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	Db	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
OC	Influenza virus A; H2N2 subtype.	Qy	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
NCBI_TaxID	135321;	Db	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
RN	SEQUENCE FROM N.A.	RESULT 12	
RA	Lindstrom S. B.	VNS1_IACHI	
RL	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.	ID	VNS1_IACHI STANDARD;
DR	EMBL; AY210152; AAO46569.1; -.	AC	P11618;
DR	HSSP; P03495; 1AII.	DT	01-OCT-1989 (Rel. 12, Created)
DR	GO; GO:003723; P:RNA binding; IEA.	DT	01-NOV-1990 (Rel. 16, Last sequence update)
DR	InterPro; IPR000256; S157NS1_bind.	DT	25-OCT-2004 (Rel. 45, Last annotation update)
DR	InterPro; IPR0009068; S157NS1_bind.	DB	Nonstructural protein NS1.
DR	Protein; P000613; Flu_NS1; 1.	GN	Name=8;
DR	SEQUENCE 237 AA; 26944 MW;	OS	Influenza A virus (strain A/Chile/1/83 H1N1)
DR	AA82935CF4533C5C CRC64;	RA	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
DR	Best Local Similarity 96.1%; Pred. No. 3.1e-88;	RN	[1]
DR	Matches 221; Conservative 5; Mismatches 4; Indels 0; Gaps 0;	RP	SEQUENCE FROM N.A.
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	RX	Medline: 83345097; PubMed: 2762132;
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRV 60	RA	Schreiber E., Roelske H., Michal S.;
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	RA	Influenza virus A.
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	NCBI_TaxID	241242;
DR	121 QAIMDKS11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	RT	"Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83 (H1N1)."
DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	RT	Nucleic Acids Res. 17:5381-5381 (1999).
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	RT	RI
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	CC	-i - ALTERNATIVE PRODUCTS:
DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	CC	Event=Alternative splicing; Named isoforms=2;
DR	NCBI_TaxID 221935;	CC	Name=NS1;
DR	1AII	CC	IsolId=P11618-1; Sequence=Displayed;
DR	1AII	CC	Name=NS2;
DR	IsolId=P11619-1; Sequence=External;	CC	IsolId=P11619-1; Sequence=External;
DR	HSSP; P03495; 1NS1.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
DR	InterPro; IPR000256; Flu_NS1.	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
DR	InterPro; IPR009068; S157NS1_bind.	CC	the European Bioinformatics Institute. There are no restrictions on its
DR	Pfam; PF06060; Flu_NS1; 1.	CC	use by non-profit institutions as long as long as its content is in no
DR	ProDom; PD00613; Flu_NS1; 1.	CC	way modified and this statement is not removed. Usage by and for commercial
DR	Alternative splicing; Non-structural protein.	CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
DR	SEQUENCE 237 AA; C33A9E3D0386E152 CRC64;	CC	EMBL; X15282; CAA33355-2;
DR	IsolId=P03495; 1NS1.	CC	DR
DR	InterPro; IPR000256; Flu_NS1.	DR	InterPro; IPR009068; S157NS1.
DR	Pfam; PF06060; Flu_NS1; 1.	DR	Pfam; PF06060; Flu_NS1; 1.
DR	ProDom; PD00613; Flu_NS1; 1.	DR	ProDom; PD00613; Flu_NS1; 1.
DR	Alternative splicing; Non-structural protein.	DR	Alternative splicing; Non-structural protein.
DR	SEQUENCE 237 AA; 26819 MW;	DR	SEQUENCE 237 AA; 26819 MW; C33A9E3D0386E152 CRC64;
DR	Query Match 96.2%; Score 1128; DB 1; Length 237;	DR	Query Match 96.2%; Score 1128; DB 1; Length 237;
DR	Best Local Similarity 95.2%; Pred. No. 2.2e-87; Indels 0; Gaps 0;	DR	Best Local Similarity 95.2%; Pred. No. 2.2e-87; Indels 0; Gaps 0;
DR	Matches 219; Conservative 7; Mismatches 4;	DR	Matches 219; Conservative 7; Mismatches 4;
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
DR	NCBI_TaxID 221935;	DR	NCBI_TaxID 221935;
DR	1AII	DR	1AII
DR	GO; GO:003723; P:RNA binding; IEA.	DR	GO; GO:003723; P:RNA binding; IEA.
DR	InterPro; IPR000256; S157NS1_bind.	DR	InterPro; IPR000256; S157NS1_bind.
DR	Pfam; PF06060; Flu_NS1; 1.	DR	Pfam; PF06060; Flu_NS1; 1.
DR	ProDom; PD00613; Flu_NS1; 1.	DR	ProDom; PD00613; Flu_NS1; 1.
DR	Alternative splicing; Non-structural protein.	DR	Alternative splicing; Non-structural protein.
DR	SEQUENCE 230 AA; 26089 MW;	DR	SEQUENCE 230 AA; 26089 MW;
DR	0A6DE9DEF3019F70 CRC64;	DR	0A6DE9DEF3019F70 CRC64;
DR	Query Match 96.3%; Score 1129; DB 2; Length 230;	DR	Query Match 96.3%; Score 1129; DB 2; Length 230;
DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;	DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;
DR	Matches 220; Conservative 6; Mismatches 4;	DR	Matches 220; Conservative 6; Mismatches 4;
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
DR	NCBI_TaxID 221935;	DR	NCBI_TaxID 221935;
DR	1AII	DR	1AII
DR	GO; GO:003723; P:RNA binding; IEA.	DR	GO; GO:003723; P:RNA binding; IEA.
DR	InterPro; IPR000256; S157NS1_bind.	DR	InterPro; IPR000256; S157NS1_bind.
DR	Pfam; PF06060; Flu_NS1; 1.	DR	Pfam; PF06060; Flu_NS1; 1.
DR	ProDom; PD00613; Flu_NS1; 1.	DR	ProDom; PD00613; Flu_NS1; 1.
DR	Alternative splicing; Non-structural protein.	DR	Alternative splicing; Non-structural protein.
DR	SEQUENCE 230 AA; 26089 MW;	DR	SEQUENCE 230 AA; 26089 MW;
DR	0A6DE9DEF3019F70 CRC64;	DR	0A6DE9DEF3019F70 CRC64;
DR	Query Match 96.3%; Score 1129; DB 2; Length 230;	DR	Query Match 96.3%; Score 1129; DB 2; Length 230;
DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;	DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;
DR	Matches 220; Conservative 6; Mismatches 4;	DR	Matches 220; Conservative 6; Mismatches 4;
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
DR	NCBI_TaxID 221935;	DR	NCBI_TaxID 221935;
DR	1AII	DR	1AII
DR	GO; GO:003723; P:RNA binding; IEA.	DR	GO; GO:003723; P:RNA binding; IEA.
DR	InterPro; IPR000256; S157NS1_bind.	DR	InterPro; IPR000256; S157NS1_bind.
DR	Pfam; PF06060; Flu_NS1; 1.	DR	Pfam; PF06060; Flu_NS1; 1.
DR	ProDom; PD00613; Flu_NS1; 1.	DR	ProDom; PD00613; Flu_NS1; 1.
DR	Alternative splicing; Non-structural protein.	DR	Alternative splicing; Non-structural protein.
DR	SEQUENCE 230 AA; 26089 MW;	DR	SEQUENCE 230 AA; 26089 MW;
DR	0A6DE9DEF3019F70 CRC64;	DR	0A6DE9DEF3019F70 CRC64;
DR	Query Match 96.3%; Score 1129; DB 2; Length 230;	DR	Query Match 96.3%; Score 1129; DB 2; Length 230;
DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;	DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;
DR	Matches 220; Conservative 6; Mismatches 4;	DR	Matches 220; Conservative 6; Mismatches 4;
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
DR	NCBI_TaxID 221935;	DR	NCBI_TaxID 221935;
DR	1AII	DR	1AII
DR	GO; GO:003723; P:RNA binding; IEA.	DR	GO; GO:003723; P:RNA binding; IEA.
DR	InterPro; IPR000256; S157NS1_bind.	DR	InterPro; IPR000256; S157NS1_bind.
DR	Pfam; PF06060; Flu_NS1; 1.	DR	Pfam; PF06060; Flu_NS1; 1.
DR	ProDom; PD00613; Flu_NS1; 1.	DR	ProDom; PD00613; Flu_NS1; 1.
DR	Alternative splicing; Non-structural protein.	DR	Alternative splicing; Non-structural protein.
DR	SEQUENCE 230 AA; 26089 MW;	DR	SEQUENCE 230 AA; 26089 MW;
DR	0A6DE9DEF3019F70 CRC64;	DR	0A6DE9DEF3019F70 CRC64;
DR	Query Match 96.3%; Score 1129; DB 2; Length 230;	DR	Query Match 96.3%; Score 1129; DB 2; Length 230;
DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;	DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;
DR	Matches 220; Conservative 6; Mismatches 4;	DR	Matches 220; Conservative 6; Mismatches 4;
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
DR	NCBI_TaxID 221935;	DR	NCBI_TaxID 221935;
DR	1AII	DR	1AII
DR	GO; GO:003723; P:RNA binding; IEA.	DR	GO; GO:003723; P:RNA binding; IEA.
DR	InterPro; IPR000256; S157NS1_bind.	DR	InterPro; IPR000256; S157NS1_bind.
DR	Pfam; PF06060; Flu_NS1; 1.	DR	Pfam; PF06060; Flu_NS1; 1.
DR	ProDom; PD00613; Flu_NS1; 1.	DR	ProDom; PD00613; Flu_NS1; 1.
DR	Alternative splicing; Non-structural protein.	DR	Alternative splicing; Non-structural protein.
DR	SEQUENCE 230 AA; 26089 MW;	DR	SEQUENCE 230 AA; 26089 MW;
DR	0A6DE9DEF3019F70 CRC64;	DR	0A6DE9DEF3019F70 CRC64;
DR	Query Match 96.3%; Score 1129; DB 2; Length 230;	DR	Query Match 96.3%; Score 1129; DB 2; Length 230;
DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;	DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;
DR	Matches 220; Conservative 6; Mismatches 4;	DR	Matches 220; Conservative 6; Mismatches 4;
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
DR	NCBI_TaxID 221935;	DR	NCBI_TaxID 221935;
DR	1AII	DR	1AII
DR	GO; GO:003723; P:RNA binding; IEA.	DR	GO; GO:003723; P:RNA binding; IEA.
DR	InterPro; IPR000256; S157NS1_bind.	DR	InterPro; IPR000256; S157NS1_bind.
DR	Pfam; PF06060; Flu_NS1; 1.	DR	Pfam; PF06060; Flu_NS1; 1.
DR	ProDom; PD00613; Flu_NS1; 1.	DR	ProDom; PD00613; Flu_NS1; 1.
DR	Alternative splicing; Non-structural protein.	DR	Alternative splicing; Non-structural protein.
DR	SEQUENCE 230 AA; 26089 MW;	DR	SEQUENCE 230 AA; 26089 MW;
DR	0A6DE9DEF3019F70 CRC64;	DR	0A6DE9DEF3019F70 CRC64;
DR	Query Match 96.3%; Score 1129; DB 2; Length 230;	DR	Query Match 96.3%; Score 1129; DB 2; Length 230;
DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;	DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;
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DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120	DR	61 GKO1VERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMLMPKQVKAGPLCIRMD 120
DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180	DR	121 QIMDN11KANFSVIFDRLETLILRAFTEGAIVEISPLPSLPGHTNEDIKNAIGV 180
DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230	DR	181 LIGGLEWNNTVRSKTLQRFAWSSNENGRPLTPKOKRMARTIRSEV 230
DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	DR	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
DR	NCBI_TaxID 221935;	DR	NCBI_TaxID 221935;
DR	1AII	DR	1AII
DR	GO; GO:003723; P:RNA binding; IEA.	DR	GO; GO:003723; P:RNA binding; IEA.
DR	InterPro; IPR000256; S157NS1_bind.	DR	InterPro; IPR000256; S157NS1_bind.
DR	Pfam; PF06060; Flu_NS1; 1.	DR	Pfam; PF06060; Flu_NS1; 1.
DR	ProDom; PD00613; Flu_NS1; 1.	DR	ProDom; PD00613; Flu_NS1; 1.
DR	Alternative splicing; Non-structural protein.	DR	Alternative splicing; Non-structural protein.
DR	SEQUENCE 230 AA; 26089 MW;	DR	SEQUENCE 230 AA; 26089 MW;
DR	0A6DE9DEF3019F70 CRC64;	DR	0A6DE9DEF3019F70 CRC64;
DR	Query Match 96.3%; Score 1129; DB 2; Length 230;	DR	Query Match 96.3%; Score 1129; DB 2; Length 230;
DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;	DR	Best Local Similarity 95.7%; Pred. No. 1.7e-87; Indels 0; Gaps 0;
DR	Matches 220; Conservative 6; Mismatches 4;	DR	Matches 220; Conservative 6; Mismatches 4;
DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA 60	DR	1 MDPTNTVSSFOYDCPFLWVKRVAQDQELGDAPEFLDRDQKSLRGGSTLGLNTETAIRA

Db 121 QAIMDRNIIILKANFSVTFDRLETLILLRAFFTPEGATVGEISPLSLPGHTNEDVNAIGV 180  
 AC Q6XTJ0; PRELIMINARY; PRT; 237 AA.  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DR EMBL; NCBI\_TaxId=220954;  
 OS Virus; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A; H2N2 subtype.  
 OC Influenza virus A; H2N2 subtype.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lindstrom S.E.; Cox N.J.; Klinov A.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AAO16577.1; -.  
 DR HSSP; P03495; 1AII.  
 DR GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu\_NS1.  
 DR InterPro; IPR000668; S157NS1\_bind.  
 DR Pfam; PF00613; Flu\_NS1; 1.  
 DR ProDom; PD000613; Flu\_NS1; 1.  
 SQ SEQUENCE 237 AA; 26940 MW; 60BBC406AFD784C9 CRC64;

Query Match 96.0%; Score 1125; DB 2; Length 237;  
 Best Local Similarity 95.2%; Pred. No. 3.9e-87;  
 Matches 219; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MDPTVSSFQVDCFLWHRKRVQDAEGLDAPFLDRDQKSLRGRGSLTGNIETAIRA 60  
 DR 1 MDPTVSSFQVDCFLWHRKRVQDAEGLDAPFLDRDQKSLRGRGSLTGNIETAIRA 60  
 AC Q84068; PRELIMINARY; PRT; 233 AA.  
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DR Nonstructural protein 1 (Fragment).  
 RA Fitch W.M.;  
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenavirus A.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Buonaguro D.A.; Nakada S.; Parvin J.D.; Krystal M.; Pallete P.;  
 RA Fitch W.M.;  
 RL Evolution of human influenza A viruses over 50 years: rapid, uniform  
 rate of change in NS gene.;  
 SCIENCE 232:980-982(1986).  
 DR EMBL; M1.2592; AAA3506.1; -.  
 DR HSSP; P03495; 1NS1.  
 DR GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu\_NS1.  
 DR InterPro; IPR000968; S157NS1\_bind.  
 DR Pfam; PF00613; Flu\_NS1; 1.  
 DR ProDom; PD000613; Flu\_NS1; 1.  
 DR Nonstructural protein.  
 SQ SEQUENCE 233 AA; 26485 MW; 1C345B24E04D617D CRC64;

Query Match 95.8%; Score 1123; DB 2; Length 233;  
 Best Local Similarity 96.9%; Pred. No. 5.6e-87;  
 Matches 219; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TVSSFQVDCFLWHRKRVQDAEGLDAPFLDRDQKSLRGRGSLTGNIETAIRAGKQI 64  
 DR 1 TVSSFQVDCFLWHRKRVQDAEGLDAPFLDRDQKSLRGRGSLTGNIETAIRAGKQI 64  
 AC Q82505; PRELIMINARY; PRT; 230 AA.  
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DR Non-structural protein 1.  
 GN Name=NS1;  
 OS Influenza A virus.  
 OC ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/WSN/40; TISSUE=Mouse;  
 RA Husak P.J.; Schlesinger R.W.;  
 RT "Replication of neurovirulent and non-neurovirulent human H1N1  
 influenza A viruses in mouse brain and nerve cell cultures: virus

RT strain-specific and host cell-dependent variations in progeny virus  
 ass.;  
 RL Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert  
 RL Wood Johnson Medical School.  
 DR EMBL; U13582; AAA21580.1; -.  
 DR HSSP; P03495; 1NS1.  
 DR GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu\_NS1.  
 DR InterPro; IPR000968; S157NS1\_bind.  
 DR Pfam; PF00600; Flu\_NS1; 1.  
 DR ProDom; PD000613; Flu\_NS1; 1.  
 SQ SEQUENCE 230 AA; 26040 MW; 03D355F2EA3AC5A8 CRC64;

Query Match 95.9%; Score 1124; DB 2; Length 230;  
 Best Local Similarity 94.8%; Pred. No. 4.6e-87;  
 Matches 218; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MDPTVSSFQVDCFLWHRKRVQDAEGLDAPFLDRDQKSLRGRGSLTGNIETAIRA 60  
 DR 1 MDPTVSSFQVDCFLWHRKRVQDAEGLDAPFLDRDQKSLRGRGSLTGNIETAIRA 60  
 AC Q84068; PRELIMINARY; PRT; 233 AA.  
 DT 01-NOV-1996 (TREMBrel. 01, Created)  
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DR Nonstructural protein 1 (Fragment).  
 RA Fitch W.M.;  
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenavirus A.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Buonaguro D.A.; Nakada S.; Parvin J.D.; Krystal M.; Pallete P.;  
 RA Fitch W.M.;  
 RL Evolution of human influenza A viruses over 50 years: rapid, uniform  
 rate of change in NS gene.;  
 SCIENCE 232:980-982(1986).  
 DR EMBL; M1.2592; AAA3506.1; -.  
 DR HSSP; P03495; 1NS1.  
 DR GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu\_NS1.  
 DR InterPro; IPR000968; S157NS1\_bind.  
 DR Pfam; PF00613; Flu\_NS1; 1.  
 DR ProDom; PD000613; Flu\_NS1; 1.  
 DR Nonstructural protein.  
 SQ SEQUENCE 233 AA; 26485 MW; 1C345B24E04D617D CRC64;

Query Match 95.8%; Score 1123; DB 2; Length 233;  
 Best Local Similarity 96.9%; Pred. No. 5.6e-87;  
 Matches 219; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TVSSFQVDCFLWHRKRVQDAEGLDAPFLDRDQKSLRGRGSLTGNIETAIRAGKQI 64  
 DR 1 TVSSFQVDCFLWHRKRVQDAEGLDAPFLDRDQKSLRGRGSLTGNIETAIRAGKQI 64

Qy	65	VERILKEESDALKNTMASAPASRYLTDMTEEMSRDWMLMPKOKVAGPLCIRMDQAIM	124
Db	61	VERILKEESDALKNTMASAPASRYLTDMTEEMSRDWMLMPKOKVAGPLCIRMDQAIM	120
Qy	125	DKSITLKKANPSVIFDRLTLLRATFEGAIVGRIISPLSPGHTNEDIKNAIGVLGG	184
Db	121	DKNITLKKANPSVIFDRLTLLRATFEGAIVGRIISPLSPGHTNEDIKNAIGVLGG	180
Qy	185	LEWNNTTVRSKTLQRFAWSNENGRRPPTPKQGRKMTIRSEV	230
Db	181	LEWNDNTTVRSKTLQRFAWSNENGRRPPTPKQGRKMTIRSEV	226

Search completed: September 22, 2005, 21:46:05  
Job time : 145.504 secs

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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:28:42 ; Search time 82.3903 Seconds

(without alignments)  
568.004 Million cell updates/sec

Title: US-10-654-737-6  
Perfect score: 607

Sequence: 1 MDPNTVSSFQDILMRISRMQ.....ALQLLVEQBI RTFSFQLI 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: GeneseqD1980s:\*
- 2: GeneseqD1990s:\*
- 3: GeneseqD2000s:\*
- 4: GeneseqD2001s:\*
- 5: GeneseqD2002s:\*
- 6: GeneseqD2003as:\*
- 7: GeneseqD2003bs:\*
- 8: GeneseqD2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	590	97.2	121	5	AEE21117	Aae21117 Influenza
2	575	94.7	121	5	AB05773	Abb05773 Influenza
3	96.5	15.9	880	4	AAB96332	Aab96332 Putative
4	96.5	15.9	880	8	ADS4313	Ad43213 Bacterial
5	86	14.2	819	4	AMM40442	Aam40442 Human pol
6	86	14.2	819	4	AMM40443	Aam40443 Human pol
7	86	14.2	819	8	ADS11970	Ad511970 Human the
8	86	14.2	819	8	ADS11971	Ad511971 Human the
9	86	14.2	819	8	ADS11969	Ad511969 Human the
10	86	14.2	819	8	ADS11968	Ad511968 Human the
11	84	13.8	122	5	AEE21128	Aae23128 Influenza
12	83.5	13.8	1179	8	ADS41964	Ad41964 Bacterial
13	83	13.8	1179	8	ADN18677	Adn18677 Bacterial
14	83	13.7	996	4	ABTB1614	Abt1614 Drosophil
15	82.5	13.6	236	7	ADN95580	Adn95580 Human BBC
16	82	13.5	350	2	AY37571	Aay37571 Chlamydia
17	82	13.5	561	2	AAW53043	Aaw53043 Streptococ
18	82	13.5	876	7	ADM26084	Adm26084 Hyperther
19	81	13.3	156	0	ADR03991	Adr03991 Mr 25K in
20	81	13.3	498	7	ADP74149	Adp74149 Human nov
21	81	13.3	653	8	ADQ66256	Adq66256 Novel hum
22	81	13.3	872	5	AO22902	Aao22902 Phosphat
23	81	13.3	872	5	ABU65076	Abu65076 Human nov
24	81	13.3	872	8	ADN61803	Adn61803 Human nov
25	81	13.3	874	5	ABP69419	Abp69419 Human

#### ALIGNMENTS

RESULT 1  
AEE23117

ID AAE23117 standard; protein; 121 AA.

XX

AC

DT

21-AUG-2002 (first entry)

XX

DE

XX

KW

XX

XX

OS

XX

Synthetic.

XX

FT

Key

Misc-difference 8. .9  
/note= "Encoded by 48-525 bases"

XX

PN

W0200224876-A2.

XX

PD

28-MAR-2002.

XX

PF

25-SEP-2001; 2001IWO-EP011087.

XX

PR

25-SEP-2000; 2000BP-00120886.

XX

PA

(POLY-) POLYMUN SCI IMMUNOLOGISCHE FORSCHUNG.

XX

PI

Katinger H, Egorov A, Perko B, Romanova J, Katinger D;

XX

DR

2002-416282/44.

DR

N-PSDB; AAD37061

XX

PS

The present invention relates to a method for isolating Vero cells with virus, combining cells with serum-free cell culture medium, incubating cells in presence of protease and nuclease, harvesting virus and preparing vaccine.

Example 4; Page 63; 90pp; English.

XX

CC

Query Match 15.9%; Score 96.5; DB 4; Length 880;  
 Best Local Similarity 27.6%; Pred. No. 0.15;  
 Matches 29; Conservative 27; Mismatches 42; Indels 7; Gaps 3;  
 Qy 20 QLG-SSEBDLNLITQFESLKLXRDSLGEAVMRMGDHLQLQRNGKWRBOLGKPE--E 75

Db 582 ELGPESVBEIN--LRIQELLEBFHDCKYVEAKKSESELRLNKLEKEKTKTLDQAFBMLAD 638  
 Qy 76 IRWLEEVRLRHLKTTENSPGTTFMQALQILLEVEOIRTFSQL 120  
 Db 639 VENETEEBKAELKDKLDESKNEBEYEEBEKRLVKEREVSSLTARL 683

RESULT 4  
 ADS43213 ID ADS43213 standard; protein; 880 AA.  
 AC ADS43213;  
 XX DT 02-DEC-2004 (first entry)  
 XX DB Bacterial polypeptide #21643.

XX Recombinant DNA construct; transformed plant; improved plant; property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 OS Bacteria.

XX US2003231675-A1.  
 XX 18-DEC-2003.  
 PD 20-FEB-2003; 2003US-00369493.  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX (CAOY/) CAO Y.  
 PA (HINKL/) HINKLE G. J.  
 PA (SLAT/) SLATER S. C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B. S.

XX PI 2004-061375/06.  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX DR 2004-061375/06.  
 PT New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX Claim 1; SEQ ID NO 21643; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a method of producing a  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC comprising transforming a plant with the recombinant DNA construct and  
 CC growing the transformed plant, where the recombinant DNA construct is  
 CC useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX SQ Sequence 880 AA;  
 Query Match 15.9%; Score 96.5; DB 8; Length 880;  
 Best Local Similarity 27.6%; Pred. No. 0.15;  
 Matches 29; Conservative 27; Mismatches 42; Indels 7; Gaps 3;  
 XX Qy 20 OLQ-SSESBDANGITQFESKURLYDSDGAVMRNGDLHSQNRRGKWRBULGQKF--B 75  
 DB 582 ELGFESVVEIN--LRIQELLEBFHDCKYVEAKKSESELRLNKLEKEKTKTLDQAFBMLAD 638  
 Qy 76 IRWLEEVRLRHLKTTENSPGTTFMQALQILLEVEOIRTFSQL 120  
 DB 639 VENETEEBKAELKDKLDESKNEBEYEEBEKRLVKEREVSSLTARL 683

RESULT 5  
 AAM40442 ID AAM40442 standard; protein; 819 AA.  
 AC AAM40442;  
 XX DT 22-OCT-2001 (first entry)  
 XX DE Human polypeptide SEQ ID NO 5373.  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX OS Homo sapiens.  
 PN WO200153312-A1.  
 XX PR 26-JUL-2001.  
 XX PR 26-DEC-2000; 2000WO-US034263.  
 XX PR 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.  
 PR 25-APR-2000; 2000US-0052317.  
 PR 20-JUN-2000; 2000US-00598012.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-0063450.  
 PR 14-SEP-2000; 2000US-00662131.  
 PR 19-OCT-2000; 2000US-00693036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX (HYSE-) HYSEQ INC.  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 PI Zhou P, Goodrich R, Drmanac RT;  
 XX DR WPI; 2001-442253/47.  
 N-PSDB; AAI59598.  
 XX PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 CC as central nervous system injuries.  
 XX Example 2; SEQ ID NO 5373; 10078pp; English.  
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
 CC encoded polypeptides (AAM3642-AAM4213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, CC Activ/inhibin activity, chemokinetic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC C.N.S disorders. Note: The sequence data for this patient did not form CC part of the printed specification

XX

SQ Sequence 819 AA;

Query Match 14.2%; Score 86; DB 4; Length 819;

Best Local Similarity 21.5%; Pred. No. 2.1; Mismatches 32; Gaps 4;

Matches 23; Conservative 32; Indels 18; Gaps 4;

CC

Db 19 MQLGSSSEDLNGITQFESLKLRYRDLIGEAVM-RMGLDLSLQNLQNGKREQLGQ-----71

QY 537 LPIGTASADVAADIAK-----YTSKLMDAIKGTMTEIYNDLSKNTWKAQLAEDSQGLR 590

QY 72 -KPEBIRWL---IEBVRHLRKITENSFPIQITFQALQQLLVEQEI 113

Db 591 IEIEKLQWHLHQELQSEMKHNLTEITMAEMRQSWEQRDRLLIAEVKKQL 637

RESULT 6

ID AAM40443 Standard; protein: 819 AA.

AC AAM40443;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 5374.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemokinetic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

XX PN 26-JUL-2001.

XX PP 26-DEC-2000; 2000WO-US034263.

XX PR 23-DBC-1999; 9905-004-1275.

PR 21-JAN-2000; 2000US-00468725.

PR 15-APR-2000; 2000US-00552317.

PR 20-TUN-2000; 2000US-00538042.

PR 19-JUL-2000; 2000US-00620312.

PR 13-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00653036.

PR 29-NOV-2000; 2000US-00727344.

XX PA (HYSEQ) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Zhao QA;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Wang Z, Ma Y, Wehrman T, Zhang J, Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Wang G, Zhou P;

XX DR WPI; 2001-442253/47.

DR N-PSDB; AAI59599.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.

XX PS Example 2; SEQ ID NO 5374; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the CC encoded polypeptides (AAM8642-AAM4213) with nootropic, CC immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide CC of the invention may be used to treat diseases of the peripheral nervous CC system, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activities such as: Immune system suppression, CC Activ/inhibin activity, chemokinetic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC C.N.S disorders. Note: The sequence data for this patient did not form CC part of the printed specification

XX SQ Sequence 819 AA;

Query Match 14.2%; Score 86; DB 4; Length 819;

Best Local Similarity 21.5%; Pred. No. 2.1; Mismatches 32; Gaps 4;

Matches 23; Conservative 32; Indels 18; Gaps 4;

CC

Db 19 MQLGSSSEDLNGITQFESLKLRYRDLIGEAVM-RMGLDLSLQNLQNGKREQLGQ-----71

QY 537 LPIGTASADVAADIAK-----YTSKLMDAIKGTMTEIYNDLSKNTWKAQLAEDSQGLR 590

QY 72 -KPEBIRWL---IEBVRHLRKITENSFPIQITFQALQQLLVEQEI 113

Db 591 IEIEKLQWHLHQELQSEMKHNLTEITMAEMRQSWEQRDRLLIAEVKKQL 637

Query Match 14.2%; Score 86; DB 4; Length 819;

Best Local Similarity 21.5%; Pred. No. 2.1; Mismatches 32; Gaps 4;

Matches 23; Conservative 32; Indels 18; Gaps 4;

CC

Db 19 MQLGSSSEDLNGITQFESLKLRYRDLIGEAVM-RMGLDLSLQNLQNGKREQLGQ-----71

QY 537 LPIGTASADVAADIAK-----YTSKLMDAIKGTMTEIYNDLSKNTWKAQLAEDSQGLR 590

QY 72 -KPEBIRWL---IEEYHLRKITENSFPIQITFQALQQLLVEQEI 113

Db 591 IEIEKLQWHLHQELQSEMKHNLTEITMAEMRQSWEQRDRLLIAEVKKQL 637

RESULT 7

ID ADS11970 standard; protein: 819 AA.

XX ADS11970;

XX DT 16-DEC-2004 (first entry)

DB Human therapeutic contig protein - SEQ ID 2207.

XX antiinflammatory; neuroprotective; antianemic; cytostatic; vulnerability;

KW inflammatory; hematopoiesis; immunity; neurodegenerative; stem cell;

KW aplastic anaemia; cancer; wound healing; gene therapy.

XX Homo sapiens.

OS Homo sapiens.

XX Key 1. 819

FT Misc-difference 1. 819

FT /label= "OTHR" /note= "OTHR = In-frame STOP codon"

XX WO2004080148-A2.

XX PD 23-SEP-2004.

XX PF 30-SEP-2003; 2003WO-US030720.

XX PR 02-OCT-2002; 2002US-0416186P.

XX PA (NUVEO) NUVEO INC.

XX PI Tang YT, Abundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y, Wehrman T, Zhang J, Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Wang G, Zhou P;

XX DR WPI; 2004-669857/65.

DR N-PSDB; ADS11372.

XX PT Polynucleotide, useful in preparing a composition for diagnosing or PT treating inflammatory, neurodegenerative or stem cell disorders, e.g., PT aplastic anemia or cancer for promoting wound healing.

PS Example 2; SEQ ID NO 2207; 718pp; English.  
 XX The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianaemic, cytostatic and vulnerability activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haemopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic contig protein of the invention.

XX sequence 819 AA;  
 Query Match 14.2%; Score 86; DB 8; Length 819;  
 Best Local Similarity 21.5%; Pred. No. 2.1;  
 Matches 32; Mismatches 34; Indels 18; Gaps 4;  
 Best Local Similarity 21.5%; Pred. No. 2.1;  
 Matches 32; Mismatches 34; Indels 18; Gaps 4;  
 Qy 19 MQLGSSSDLNLGIIQFESLKLRYRDGLAVM-RMGDLSLQNRNGKREQLGQ-----71  
 Db 537 LPIGTASADVAADIAK-----YTSKLMDAIKGTMTEYNDLSKNTWKAQLAEDSQCLR 590  
 Qy 72 -KPEEIRWL---IEEVHRHLKITENSPEQITFMQALQOLLLVEQEI 113  
 Db 591 IEIEKLQWHLQOELSEMKHNLTEMAENRQSWEQERDLIAEVRKQL 637

RESULT 9  
 ADS11959  
 ID ADS11959 standard; protein 819 AA.  
 XX  
 AC ADS11959;  
 AC ADS11959;  
 XX  
 DT 16-DEC-2004 (first entry)

XX Human therapeutic contig protein - SEQ ID 2206.  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DB Human therapeutic contig protein - SEQ ID 2208.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerability; KW inflammatory; haemopoiesis; immunity; neurodegenerative; 'stem cell'; KW aplastic anaemia; cancer; wound healing; gene therapy.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Misc-difference 1:819  
 FT /label= Unknown, OTHER  
 FT /note= "OTHER = In-Frame STOP codon"  
 XX  
 WO2004080148-A2.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PN 30-SEP-2003; 2003WO-US030720.  
 XX  
 PN 02-OCT-2002; 2002US-0416186P.  
 XX  
 PA (NUVE-) NUVELO INC.

XX  
 PP Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
 XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
 XX  
 DR WPI: 2004-668857/65.  
 DR N-PSDB; ADS11373.  
 XX  
 PT New polynucleotide, useful in preparing a composition for diagnosing or  
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
 PT aplastic anaemia or cancer for promoting wound healing.  
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 PS Example 2; SEQ ID NO 2208; 718pp; English.  
 DR N-PSDB; ADS11373.

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 PS Example 2; SEQ ID NO 2208; 718pp; English.  
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 PT The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianaemic, cytostatic and vulnerability activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haemopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic contig

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 CC procedures. The current sequence is that of a human therapeutic contig  
 CC protein of the invention.  
 XX  
 SQ Sequence 819 AA;

Query Match 14.2%; Score 86; DB 8; Length 819;  
 Best Local Similarity 21.5%; Pred. No. 2.1;  
 Matches 32; Mismatches 34; Indels 18; Gaps 4;  
 Best Local Similarity 21.5%; Pred. No. 2.1;  
 Matches 32; Mismatches 34; Indels 18; Gaps 4;

Qy 19 MQLGSSSDLNLGIIQFESLKLRYRDGLAVM-RMGDLSLQNRNGKREQLGQ-----71  
 Db 537 LPIGTASADVAADIAK-----YTSKLMDAIKGTMTEYNDLSKNTWKAQLAEDSQCLR 590  
 Qy 72 -KPEEIRWL---IEEVHRHLKITENSPEQITFMQALQOLLLVEQEI 113  
 Db 591 IEIEKLQWHLQOELSEMKHNLTEMAENRQSWEQERDLIAEVRKQL 637

RESULT 9  
 ADS11959  
 ID ADS11959 standard; protein 819 AA.  
 XX  
 AC ADS11959;  
 AC ADS11959;  
 XX  
 DT 16-DEC-2004 (first entry)

XX Human therapeutic contig protein - SEQ ID 2206.  
 XX  
 DB Human therapeutic contig protein - SEQ ID 2208.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerability; KW inflammatory; haemopoiesis; immunity; neurodegenerative; 'stem cell'; KW aplastic anaemia; cancer; wound healing; gene therapy.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH  
 FT Misc-difference 1:819  
 FT /label= Unknown, OTHER  
 FT /note= "OTHER = In-Frame STOP codon"  
 XX  
 WO2004080148-A2.  
 XX  
 PN WO2004080148-A2.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PN 30-SEP-2003; 2003WO-US030720.  
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CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX Sequence 1179 AA;

Query Match 13.8%; Score 83.5; DB 8; Length 1179;  
 Best Local Similarity 23.9%; Pred. No. 6; 6; Indels 15; Gaps 3;  
 Matches 27; Conservative 27; Mismatches 44; Indels 15; Gaps 3;

Qy 23 SSESDELLITQF-----ESLKYRDSLGEAVMRMQLHSIQRNQKWRQLGQ 71  
 Db 825 SLEEEELVNKINALKANINNEALKSLTLEKKEKEIYRSIEEQKCKEBELR 84  
 Qy 72 KFFBIRNLIEEHR--LKITENSFEOITFNGQALQOLLEVEBIRTFSPQL 121  
 Db 885 KVAELREKEKISRRIQSLRIVFNTL-KVRNSQQLSLIMENKSQQLKFSKEVYI 936

RESULT 14

ABB71614

ID ABB71614 standard; protein; 996 AA.

AC ABB71614;

XX 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 41634.

XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX pharmaceutical.

XX Drosophila melanogaster.

XX 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX XX WPI; 2001-656860/75.

XX DR N-PSDB; ABL15717.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.

XX Disclosure; SEQ ID NO 41634; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL6175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC Printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 996 AA;  
 Query Match 13.7%; Score 83; DB 4; Length 996;  
 Best Local Similarity 26.1%; Pred. No. 6;  
 Matches 31; Conservative 25; Mismatches 39; Indels 24; Gaps 5;  
 Qy 2 DPNTVSSFDITLIRISKMQLQGSSSBPLNGITQFESLKLYRDSLGEAVMRGDLH----56  
 Db 824 DPEQI --QQQLQSVLQ--SGCLEG----ETLQMMTDGSGQMVLRGDNNBQLI 872  
 Qy 57 --SLQRNGKWRQEOLGQKFRBIRNLIEEHRRLKITENSFPEQITFMQALQOLLEVEQI 113  
 Db 873 DASLNLSEGQLIQQCQDGEAHHVSEDGTRIPV-----VSYTEDGQPIVQVQQV 925

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Qy 2 DPNTVSSFDITLIRISKMQLQGSSSBPLNGITQFESLKLYRDSLGEAVMRGDLH----56  
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 Best Local Similarity 26.1%; Pred. No. 6;  
 Matches 31; Conservative 25; Mismatches 39; Indels 24; Gaps 5;

Qy 2 DPNTVSSFDITLIRISKMQLQGSSSBPLNGITQFESLKLYRDSLGEAVMRGDLH----56  
 Db 824 DPEQI --QQQLQSVLQ--SGCLEG----ETLQMMTDGSGQMVLRGDNNBQLI 872

Qy 57 --SLQRNGKWRQEOLGQKFRBIRNLIEEHRRLKITENSFPEQITFMQALQOLLEVEQI 113  
 Db 873 DASLNLSEGQLIQQCQDGEAHHVSEDGTRIPV-----VSYTEDGQPIVQVQQV 925

XX Query Match 13.7%; Score 83; DB 4; Length 996;  
 Best Local Similarity 26.1%; Pred. No. 6;  
 Matches 31; Conservative 25; Mismatches 39; Indels 24; Gaps 5;

Qy 2 DPNTVSSFDITLIRISKMQLQGSSSBPLNGITQFESLKLYRDSLGEAVMRGDLH----56  
 Db 824 DPEQI --QQQLQSVLQ--SGCLEG----ETLQMMTDGSGQMVLRGDNNBQLI 872

Qy 57 --SLQRNGKWRQEOLGQKFRBIRNLIEEHRRLKITENSFPEQITFMQALQOLLEVEQI 113  
 Db 873 DASLNLSEGQLIQQCQDGEAHHVSEDGTRIPV-----VSYTEDGQPIVQVQQV 925

XX Query Match 13.7%; Score 83; DB 4; Length 996;  
 Best Local Similarity 26.1%; Pred. No. 6;  
 Matches 31; Conservative 25; Mismatches 39; Indels 24; Gaps 5;

Qy 2 DPNTVSSFDITLIRISKMQLQGSSSBPLNGITQFESLKLYRDSLGEAVMRGDLH----56  
 Db 824 DPEQI --QQQLQSVLQ--SGCLEG----ETLQMMTDGSGQMVLRGDNNBQLI 872

CC VEGP-D polypeptides and polynucleotides. The invention may be useful for  
 CC the development of compounds with an antiangiogenic, cytostatic,  
 CC vasoconstrictive or antiinflammatory activity or for gene therapy. The method  
 CC is useful in modulating the growth or differentiating activity of blood  
 CC endothelial cells or lymphatic endothelial cells, in treating hereditary  
 CC lymphoedema, in screening for an endothelial cell disorder or  
 CC predisposition to the disorder or in monitoring the efficacy or toxicity  
 CC of a drug on endothelial cells. The agent is useful in manufacturing a  
 CC medicament for the differential modulation of blood vessel endothelial  
 CC cell or lymphatic vessel endothelial cell growth or differentiation. The  
 CC lymphatic growth agent may also be used in manufacturing a medicament for  
 CC the treatment of hereditary lymphoedema resulting from mutation in a  
 CC LBC gene or other diseases involving the lymphatic vessels, such as  
 CC various inflammatory diseases and cancer metastasis via the lymphatic  
 CC system. The present sequence is that of a human LEC/BEC differentially  
 CC expressed protein which is related to the method of the invention. Note:  
 CC This sequence does not appear in the specification but was obtained by:  
 CC the indexer using the source data given in table 14 of the specification.  
 XX

SQ Sequence 236 AA;

Query Match 13.6%; Score 82.5; DB 7; Length 236;

Best Local Similarity 32.0%; Pred. No. 0.94; Matches 32; Conservative 16; Mismatches 29; Indels 23; Gaps 5;

Qy	3 PNTVSSFQDILMRISKMQLGSSSEDLNGITQFESIILKLYRDSDLGRAVMRM--GDLHSLQN 60
Db	23 PYPPSNRYETLILKORHVLQIGRSIDINRLTQRISSAMYK-SLDGDAISRFESEDITSI-- 79
Qy	61 RNGKWRQLGKQFEEIRWIL--EVPHRL--KITENSFE 95
Db	80 -----VELEWLEINRVTHRLCKHMTLDSPD 106

Search completed: September 22, 2005, 21:42:25  
 Job time : 86.3903 secs

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4 protein - protein search, using sw model

on September 22, 2005, 21:33:28 ; Search time 16.8917 Seconds  
(without alignment) 60.225 Million cell "undates/none"

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perfect score: 607.

Scanning table: **base59182**    **Ganon 10.0**    **Ganext 0.5**

searched: 283416 9809 96216763 residues

תְּנִשְׁאָרָה בְּבָבִילוֹן

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Maximum Match 100%

available : <http://www.astro.ub.edu/~perez/astro/astro.html>

\* 1  
N  
H  
H  
P  
P  
N  
C

4 : **Pir4:**\*

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

בְּרָאָמָר

Query		Match		Length		DB		ID		Description	
built No.	Score	Query	Match	Length	DB	ID					
1	597	98.4	121	1	MNIV2A					nonstructural prot	
	2	596	98.2	121	2	S33655				nonstructural prot	
3	594	97.9	121	1	MNIV62					nonstructural prot	
4	588	96.9	121	1	MNIV2M					nonstructural prot	
5	587	96.7	121	1	MNIVC2					nonstructural prot	
6	586	96.5	121	1	MNIV2W					nonstructural prot	
7	575	94.7	121	1	E45539					nonstructural prot	
8	575	94.7	121	1	MNIV2K					nonstructural prot	
9	574	94.6	121	2	S09649					NS2 protein - infl	
10	569	93.7	118	1	MNIVX					nonstructural prot	
11	567	93.4	121	1	MNIV2					nonstructural prot	
12	564	92.9	118	1	MNIVX4					nonstructural prot	
13	564	92.9	118	1	MNIVX8					nonstructural prot	
14	564	92.9	121	1	MNIVB4					nonstructural prot	
15	563	92.8	121	1	MNIVB1					nonstructural prot	
16	559	92.1	121	1	MNIVB3					nonstructural prot	
17	556	91.6	118	1	MNIVX2					nonstructural prot	
18	549	90.4	118	1	MNIVX6					nonstructural prot	
19	517	85.2	108	1	MNIV2F					nonstructural prot	
20	486	80.1	121	1	MNIV26					nonstructural prot	
21	478	78.7	121	2	B45575					nonstructural prot	
22	475	78.3	121	1	MNIVB7					nonstructural prot	
23	473	77.9	121	1	MNIVB5					nonstructural prot	
24	468	77.1	121	1	MNIVB6					nonstructural prot	
25	467	76.9	121	1	MNIVB8					nonstructural prot	
26	96.5	15.9	880	2	F75103					conserved hypothetical	
27	88	14.5	2541	2	T29340					hypothetical prote	
28	83.5	13.8	1179	2	MNIVR					probable chromosomal	
29	82.5	13.6	122	1						nonstructural protein	

			nonstructural prot
			22K surface membra
			apolipoprotein A-I
			Paramyosin - fluke
			Spindle pole body
			hypothetical prote
			VSG expression sit
			outer dynein arm d
			interactin - slime
			hypothetical prote
			GTP diphosphokinase
30	81.5	13.4	MNTV23
		122	1
31	81	13.3	A45553
32	81	13.3	S29555
33	80.5	13.3	A60508
34	80.5	13.3	S26710
35	80	13.2	T3209
36	80	13.2	T47145
37	80	13.2	T51924
38	80	13.2	T32574
39	80	13.2	T46248
40	79.5	13.1	E83947
41	79	13.0	B32433
42	79	13.0	T08401
43	79	13.0	T14667
44	79	13.0	T45503
	78.5	12.9	E82657
		71.8	

ALIGNMENT

```

RESULT 1
MNIV2A
nonstructural protein NS2 - influenza A virus (strain A/USSR/90/77 [H1N1])
C;Species: influenza A virus
C;Date: 31-Oct-1980 #sequence revision 14-Nov-1983 #text_change 16-Jul-1999
C;Accession: B2991; A04095; 990801; C9991; D92991
R;Krytay, M.; Buonagurio, D.; Young, J.F.; Palese, P.
J;Virol. 45: 547-554, 1983
A;Title: Sequential mutations in the NS genes of influenza virus field strains.
A;Reference number: A92991; PMID:83164298; PMID:6834468
A;Accession: B2991
A;Molecule type: genomic RNA
A;Residues: 1-121 <CRY>
A;Cross-references: GB:K00578; NID:q324839; PIDN:AAA43539.1; PID:g324840
C;Genetics:
C;Superfamily: influenza virus nonstructural protein NS2
C;Keywords: alternative splicing

Query Match 98.4%; Score 597; DB 1; Length 121;
Best Local Similarity 97.3%; Pred. No. 2.6e-44;
Matches 118; Conservative 2; N mismatches 1; Indels 0; Gaps 0;
Oy 1 MDPNTSSFQILMRSKMQGSSSSDNLNITQPBSLKYRDLTSLGEAVNRMGDLISLQN 60
Db 1 MDPNTSSFQILMRSKMQGSSSSDNLNITQPBSLKYRDLTSLGEAVNRMGDLISLQN 60
Qy 61 RNGKNEFQLGKPFEEIRWLLIEEVHRHLKITENSPQQITENQALQQLLEVBOBIRTSFSQL 120
Db 61 RNGKNEFQLGKPFEEIRWLLIEEVHRHLKITENSPQQITENQALQQLLEVFEVQEIRTSFSQL 120

```

**RESULT 2**

S33685 nonstructural protein NS1 - influenza A virus (strain A/WS/33)  
 C;Species: influenza A virus  
 A;Variety: strain A/WS/33  
 C;Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
 C;Accession: S33685; S32221  
 R;Ward, A.C.; Azad, A.A.; MacCreadie, I.G.; McKimm-Breschkin, J.L.  
 Nucleic Acids Res. 22:257, 1993  
 A;Title: Complete nucleotide sequence of the non-structural gene of the human influenza  
 A;Reference number: S33685; MNUID:93275755; PMID:8502573  
 A;Accession: S33685  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-121 <A/R>  
 A;Cross-references: UNIPROT:006049; EMBL:Z21498; NID:G296585; PIDN:CAA79707; 1; PID:q2965

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

C;Genetics:

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

Query Match 98.2%; Score 596; DB 2; Length 121;  
Best Local Similarity 98.3%; Pred. No. 3.1e-44;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;Qy 1 MDPTVSSFQDILRISKMQLGSSSDEDINGITOFESLKLRYDSLGEAVMRGMDLHSQN 60  
Db 1 MDPTVSSFQDILRMSKRNQLGSSSDEDINGITOFESLKLRYDSLGEAVMRGMDLHSQN 60  
Qy 61 RNGKWRQLGQKFBEIRWLIEVRHRLKITENSSEQITPMQALQLLVEQEIRTFPSQL 120  
Db 61 RNEKWRQLGQKFBEIRWLIEVRHRLKITENSSEQITPMQALQLLVEQEIRTFPSQL 120  
Qy 121 I 121  
Db 121 I 121

## RESULT 3

MNIV62 nonstructural protein NS2 - influenza A virus (strain A/Ann Arbor/6/60 [H2N2])

C;Species: influenza A virus

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999

C;Accession: H31831

R;Cox, N.J.; Kitame, F.; Kendal, A.P.; Maassab, H.F.; Naeve, C.

Virology 167, 545-567, 1988

A;Title: Identification of sequence changes in the cold-adapted, live attenuated influenza A virus

A;Reference number: A31831; MUID:89073759; PMID:2974219

A;Accession: H31831

A;Molecule type: genomic RNA

A;Residues: 1-121 &lt;COX&gt;

A;Cross-references: GB:M23968; GB:J04349; GB:M23969; NID:9324860; PID:9

C;Genetics:

A;Map position: segment 8

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing; nonstructural protein

Query Match 97.9%; Score 594; DB 1; Length 121;  
Best Local Similarity 96.7%; Pred. No. 4.6e-44;  
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;Qy 1 MDPTVSSFQDILRISKMQLGSSSDEDINGITOFESLKLRYDSLGEAVMRGMDLHSQN 60  
Db 1 MDPTVSSFQDILRMSKRNQLGSSSDEDINGITOFESLKLRYDSLGEAVMRGMDLHSQN 60  
Qy 61 RNGKWRQLGQKFBEIRWLIEVRHRLKITENSSEQITPMQALQLLVEQEIRTFPSQL 120  
Db 61 RNEKWRQLGQKFBEIRWLIEVRHRLKITENSSEQITPMQALQLLVEQEIRTFPSQL 120  
Qy 121 I 121  
Db 121 I 121

## RESULT 4

MNIV2M nonstructural protein NS2 - influenza A virus (strain A/FW/1/50 [H1N1])

C;Species: influenza A virus

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 16-Jul-1999

C;Accession: D92991; A04095

R;Crystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83162298; PMID:6834468

A;Accession: C92991

A;Molecule type: genomic RNA

A;Cross-references: GB:K00576; NID:9324813; PID:9324814

A;Residues: 1-121 &lt;KRY&gt;

A;Cross-references: GB:K00576; NID:9324813; PID:9324814

A;Accession: C92991

A;Molecule type: genomic RNA

A;Residues: 1-121 &lt;KRY&gt;

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS2

Query Match 96.9%; Score 588; DB 1; Length 121;  
Best Local Similarity 95.9%; Pred. No. 1.5e-43;  
Matches 116; Conservative 2; Mismatches 3; Indels 0; Gaps 0;Qy 1 MDPTVSSFQDILRISKMQLGSSSDEDINGITOFESLKLRYDSLGEAVMRGMDLHSQN 60  
Db 1 MDPTVSSFQDILRMSKRNQLGSSSDEDINGITOFESLKLRYDSLGEAVMRGMDLHSQN 60  
Qy 61 RNGKWRQLGQKFBEIRWLIEVRHRLKITENSSEQITPMQALQLLVEQEIRTFPSQL 120  
Db 61 RNEKWRQLGQKFBEIRWLIEVRHRLKITENSSEQITPMQALQLLVEQEIRTFPSQL 120  
Qy 121 I 121  
Db 121 I 121

## RESULT 5

MNIVC2 nonstructural protein NS2 - influenza A virus (strain A/Chile/1/83 [H1N1])

C;Species: influenza A virus

C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 16-Jul-1999

C;Accession: B34215; S04837

R;Schreier, E.; Roesel, H.; Michel, S.

Nucleic Acids Res. 17, 5381, 1989

A;Title: Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83 (H1N1).

A;Reference number: A34215; MUID:89345097; PMID:2762132

A;Accession: B34215

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-121 &lt;SCB&gt;

A;Cross-references: EMBL:X15282; NID:960479; PIDN:CAA33356.1; PMID:960481

C;Genetics:

A;Map position: segment 8

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing; nonstructural protein

Query Match 96.7%; Score 587; DB 1; Length 121;  
Best Local Similarity 95.9%; Pred. No. 1.8e-43;  
Matches 116; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

## RESULT 6

MNIV2W nonstructural protein NS2 - influenza A virus (strain A/FW/1/50 [H1N1])

C;Species: influenza A virus

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 24-Sep-1999

C;Accession: C92991; A04095

R;Crystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83162298; PMID:6834468

A;Accession: C92991

A;Molecule type: genomic RNA

A;Cross-references: 1-121 &lt;KRY&gt;

A;Residues: 1-121 &lt;KRY&gt;

A; Cross-references: GB:K00577; NID:9324608; PID:AAA435521.1; PID:9324809  
 A; Experimental source: strain A/Alaska/6/77  
 C; Genomics:  
 A; Map position: segment 8  
 C; Superfamily: influenza virus nonstructural protein NS2  
 C; Keywords: alternative splicing

Query Match 96.5%; Score 586; DB 1; Length 121;  
 Best Local Similarity 95.9%; Pred. No. 2.e-43;  
 Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 A; Residues: 1-121 <LAM>

Qy 1 MDPTVSSFDLIRISKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 Db 1 MDPTVSSFDLIRMSKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 A; Accession: A90801  
 A; Map type: genomic RNA  
 C; Genetics:  
 A; Introns: 10/3  
 C; Superfamily: influenza virus nonstructural protein NS2  
 C; Keywords: alternative splicing

Query Match 94.7%; Score 575; DB 1; Length 121;  
 Best Local Similarity 94.2%; Pred. No. 2.e-42;  
 Matches 114; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 A; Residues: 1-121 <LAM>

Qy 1 MDPTVSSFDLIRISKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 Db 1 MDPTVSSFDLIRMSKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 A; Accession: A90801  
 A; Map type: genomic RNA  
 C; Genetics:  
 A; Introns: 10/3  
 C; Superfamily: influenza virus nonstructural protein NS2  
 C; Keywords: alternative splicing

Query Match 94.7%; Score 575; DB 1; Length 121;  
 Best Local Similarity 94.2%; Pred. No. 2.e-42;  
 Matches 114; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 A; Residues: 1-121 <LAM>

Qy 1 MDPTVSSFDLIRISKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 Db 1 MDPTVSSFDLIRMSKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 A; Accession: A90801  
 A; Map type: genomic RNA  
 C; Genetics:  
 A; Introns: 10/3  
 C; Superfamily: influenza virus nonstructural protein NS2  
 C; Keywords: alternative splicing

RESULT 7  
 B45539 nonstructural protein NS2 - influenza A virus (strain A/chicken/Brescia/1902 [H7N7])  
 C; Species: influenza A virus  
 C; Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 26-May-1994  
 C; Accession: B45539  
 R; Klimov, A.; Prosch, S.; Schafer, J.; Bucher, D.  
 Arch. Virol. 122, 143-161, 1992  
 A; Title: Subtype H7 influenza viruses: comparative antigenic and molecular analysis of  
 A; Reference number: A45539; MUID:92109567; PMID:1530908  
 A; Accession: B45539  
 A; Map type: genomic RNA  
 A; Note: sequence extracted from NCBI backbone (NCBIN:74250, NCBIPI:74255)

A; Map position: segment 8  
 C; Superfamily: influenza virus nonstructural protein NS2  
 C; Keywords: alternative splicing

Query Match 94.7%; Score 575; DB 1; Length 121;  
 Best Local Similarity 94.2%; Pred. No. 2.e-42;  
 Matches 114; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 A; Residues: 1-121 <LAM>

Qy 1 MDPTVSSFDLIRISKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 Db 1 MDPTVSSFDLIRMSKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 A; Accession: B45539  
 A; Map type: genomic RNA  
 C; Genetics:  
 A; Introns: 10/3  
 C; Superfamily: influenza virus nonstructural protein NS2  
 C; Keywords: alternative splicing

Query Match 94.6%; Score 574; DB 2; Length 121;  
 Best Local Similarity 94.2%; Pred. No. 2.e-42;  
 Matches 114; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 A; Residues: 1-121 <LAM>

Qy 1 MDPTVSSFDLIRISKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 Db 1 MDPTVSSFDLIRMSKMQLGSSSEDLNGITOPESKLKYRDLGSAVMRGDLHSLQN 60  
 A; Accession: B45539  
 A; Map type: genomic RNA  
 C; Genetics:  
 A; Introns: 10/3  
 C; Superfamily: influenza virus nonstructural protein NS2  
 C; Keywords: alternative splicing

RESULT 8  
 MNIV2K nonstructural protein NS2 - influenza A virus (strains A/Alaska/6/77 and A/udorn/72 [H3N2])  
 C; Species: influenza A virus  
 A; Note: host Homo sapiens (man)  
 C; Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 09-Jul-2004  
 C; Accession: A04094; A90801; A04095  
 R; Buonagurio, D.A.; Krystal, M.; Palese, P.; DeBorde, D.C.; Maassab, H.F.  
 J. Virol. 49, 418-425, 1984  
 A; Title: Analysis of an influenza A virus mutant with a deletion in the NS segment.  
 A; Reference number: A92994; MUID:84115066; PMID:6363726  
 A; Accession: A04044  
 A; Map type: genomic RNA  
 A; Residues: 1-121 <BUO>

RESULT 10  
 MNIV2K nonstructural protein NS2 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fr.)

C;Species: influenza A virus  
 C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
 C;Accession: A3086  
 R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
 Virology 158, 465-468, 1987  
 A;Title: Genetic divergence of the NS genes of avian influenza viruses.  
 A;Reference number: A94361; MUID:87236215; PMID:2954302  
 A;Accession: D27846  
 A;Molecule type: Genomic RNA  
 A;Residues: 1-118 <NAK>  
 A;Cross-references: GB:MI6563; NID:9324786; PIDN:AAA43511.1; PMID:9324788  
 C;Genetics:  
 A;Gene: NS2  
 A;Map position: segment 8  
 A;Introns: 7/3  
 C;Superfamily: influenza virus nonstructural protein NS2  
 C;Keywords: alternative splicing; nonstructural protein  
 A;Map position: segment 8  
 A;Introns: 7/3  
 C;Superfamily: influenza virus nonstructural protein NS2  
 C;Keywords: alternative splicing; nonstructural protein  
 Query Match 93.7%; Score 569; DB 1; Length 118;  
 Best Local Similarity 95.8%; Pred. No. 6 2e-42; Indels 0; Gaps 0;  
 Matches 113; Conservative 4; Mismatches 1; Indels 1; Gaps 0;  
 Qy 4 NTVSSFQDILRISKWLGSSSBDINGITQFESKLKYRDSLGEAVMRMGDLHSQNNG 63  
 Db 1 NTVSSFQDILRISKWLGSSSBDINGITQFESKLKYRDSLGEAVMRMGDLHSQNNG 60  
 Qy 64 KWREQLGQKEEIRMLIEEVRLKITENSFEQTFMQALQLLVEQEIRTFSPOLI 121  
 Db 61 KWREQLGQKEEIRMLIEEVRLKITENSFEQTFMQALQLLVEQEIRTFSPOLI 118  
 RESULT 13  
 MN1VA8  
 nonstructural protein NS2 - influenza A virus (strain A/Duck/Ukraine/63 [H3N8]) (fragment  
 C;Species: influenza A virus  
 C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
 C;Accession: H27846  
 R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
 Virology 15, 465-468, 1987  
 A;Title: Genetic divergence of the NS genes of avian influenza viruses.  
 A;Reference number: A94361; MUID:87236215; PMID:2954302  
 A;Accession: H27846  
 A;Molecule type: Genomic RNA  
 A;Residues: 1-118 <NAK>  
 A;Cross-references: GB:MI6565; NID:9324789; PIDN:AAA43513.1; PMID:9324791  
 C;Genetics:  
 A;Gene: NS2  
 A;Map position: segment 8  
 A;Introns: 7/3  
 C;Superfamily: influenza virus nonstructural protein NS2  
 C;Keywords: alternative splicing; nonstructural protein  
 Query Match 92.9%; Score 564; DB 1; Length 118;  
 Best Local Similarity 94.9%; Pred. No. 1.7e-41; Indels 0; Gaps 0;  
 Matches 112; Conservative 5; Mismatches 1; Indels 1; Gaps 0;  
 Qy 4 NTVSSFQDILRISKWLGSSSBDINGITQFESKLKYRDSLGEAVMRMGDLHSQNNG 63  
 Db 1 NTVSSFQDILRISKWLGSSSBDINGITQFESKLKYRDSLGEAVMRMGDLHSQNNG 60  
 Qy 64 KWREQLGQKEEIRMLIEEVRLKITENSFEQTFMQALQLLVEQEIRTFSPOLI 121  
 Db 61 KWREQLGQKEEIRMLIEEVRLKITENSFEQTFMQALQLLVEQEIRTFSPOLI 118  
 RESULT 14  
 MN1VA8  
 nonstructural protein NS2 - influenza A virus (strain A/pintail/Alberta/119/79)  
 C;Species: influenza A virus  
 C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 08-Apr-1994  
 C;Accession: H32662  
 R;Tranor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.  
 Virology 171, 1-9, 1989  
 A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, at  
 A;Reference number: A32662; MUID:89299445; PMID:2525836  
 A;Accession: H32662

RESULT 11  
 MN1V2  
 nonstructural protein NS2 - influenza A virus (strain A/PR/8/34)  
 C;Species: influenza A virus  
 C;Date: 30-Apr-1981 #sequence\_revision 30-Apr-1981 #text\_change 16-Jul-1999  
 C;Accession: A0096  
 R;Baer, M.; Tazara, J.J.; Young, J.F.; Palese, P.; Reisfeld, A.; Skalka, A.M.  
 Nucleic Acids Res. 8, 5845-5855, 1980  
 A;Title: Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and compa  
 A;Reference number: A93714; MUID:81124304; PMID:7465426  
 A;Accession: A0096  
 A;Molecule type: Genomic RNA  
 A;Residues: 1-121  
 A;Cross-references: GB:V01104; NID:960803; PIDN:CAA24293.1; PID:960805  
 C;Genetics:  
 A;Map position: segment 8  
 C;Superfamily: influenza virus nonstructural protein NS2  
 C;Keywords: alternative splicing  
 Query Match 93.4%; Score 567; DB 1; Length 121;  
 Best Local Similarity 93.4%; Pred. No. 9 4e-42; Indels 0; Gaps 0;  
 Matches 113; Conservative 4; Mismatches 4; Indels 4; Gaps 0;  
 Qy 1 MDPNTVSSFQDILRISKWLGSSSBDINGITQFESKLKYRDSLGEAVMRMGDLHSQN 60  
 Db 1 MDPNTVSSFQDILRISKWLGSSSBDINGITQFESKLKYRDSLGEAVMRMGDLHSQN 60  
 Qy 61 RNGKWRQLGQKEEIRWLIEEVRLKITENSFEQTFMQALQLLVEQEIRTFSPOLI 120  
 Db 61 RNBKWRQLGQKEEIRWLIEEVRLKITENSFEQTFMQALQLLVEQEIRTFSPOLI 120  
 Qy 121 I 121  
 Db 121 I 121  
 RESULT 12  
 MN1VA4  
 nonstructural protein NS2 - influenza A virus (strain A/Duck/England/56 [H1N1]) (fragme  
 C;Species: influenza A virus  
 C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
 C;Accession: D27846

A;Molecule type: genomic RNA  
 A;Residues: 1-121 <TR>  
 C;Genetics:

A;Gen: NS2

A;Map position: segment 8

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing; nonstructural protein

Query Match 92.9%; Score 564; DB 1; Length 121;  
 Best Local Similarity 93.4%; Pred. No. 1.7e-41;  
 Matches 113; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDQDLRISKMQLGSSSDDLNGITQFESLKLRYDSDIGEAVNRMGDLHSQN 60  
 Db 1 MDSNTVSSFDQDLRISKMQLGSSSDDLNGITQFESLKLRYDSDIGEAVNRMGDLHSQN 60

Qy 61 RNGKWRPQLGKPEEIRWLIEEVRLKITENSFQITMQLQLLVEQIRTFPSFQL 120  
 Db 61 RNGKWRPQLSQRKFEEIRWLIEEVRLKITENSFQITMQLQLLVEQIRTFPSFQL 120

Qy 121 I 121

Db 121 I 121

#### RESULT 15

MNIVB1 nonstructural protein NS2 - influenza A virus (strains A/pintail/Alberta/268/78 and A/mal-

C;Species: influenza A virus  
 C;Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text\_change 19-Oct-1995

C;Accession: B32662; D32662

R;Treadnor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.

Virology 171, 1-9, 1989

A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, a

A;Reference number: A32662; MUID:89299445; PMID:2525836

A;Molecule type: genomic RNA

A;Residues: 1-121 <TR>

A;Experimental source: strain A/pintail/Alberta/268/78

A;Accession: D32662

A;Molecule type: genomic RNA

A;Residues: 1-121 <TR>

A;Experimental source: strain A/mallard/New York/6750/78

C;Genetics:

A;Gen: NS2

A;Map position: segment 8

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing; nonstructural protein

Query Match 92.8%; Score 563; DB 1; Length 121;  
 Best Local Similarity 93.4%; Pred. No. 2.1e-41;  
 Matches 113; Conservative 3; Mismatches 5; Indels 0; Gaps 0; Gaps 0;

Qy 1 MDPNTVSSFDQDLRISKMQLGSSSDDLNGITQFESLKLRYDSDIGEAVNRMGDLHSQN 60  
 Db 1 MDSNTVSSFDQDLRISKMQLGSSSDDLNGITQFESLKLRYDSDIGEAVNRMGDLHSQN 60

Qy 61 RNGKWRPQLGKPEEIRWLIEEVRLKITENSFQITMQLQLLVEQIRTFPSFQL 120  
 Db 61 RNGKWRPQLSQRKFEEIRWLIEEVRLKITENSFQITMQLQLLVEQIRTFPSFQL 120

Qy 121 I 121

Db 121 I 121

Scoring table:	BL03DN62										
Gapop 10.0 , Gapext 0.5											
Searched:	1612378 seqs, 512079187 residues										
Total number of hits satisfying chosen parameters:	1612378										
Minimum DB seq length: 0											
Maximum DB seq length: 2000000000											
Post-processing:	Minimum Match 0% Maximum Match 100%										
Listing first 45 summaries											
Database :	UniProt_03_*										
1: uniprot_sprot:*											
2: uniprot_trembl:*											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
Result No.	Score	Query	Match	Length	DB	ID	Description				
1	604	99.5	121	2	Q89733		Q89733 influenza a				
2	600	98.8	121	2	Q67248		Q67248 influenza a				
3	597	98.4	121	1	VNS2_IAUSS		P03504 influenza a				
4	596	98.2	121	2	Q0649		P06049 influenza a				
5	594	97.9	121	1	VNS2_IAANN		P21432 influenza a				
6	594	97.9	121	2	Q6XTU1		Q6xtu1 influenza a				
7	594	97.9	121	2	Q6XTU7		Q6xtu7 influenza a				
8	590	97.2	121	1	VNS2_IALB2		P26133 influenza a				
9	590	97.2	121	2	Q67264		Q67264 influenza a				
10	590	97.2	121	2	Q6XTU9		Q6xtu9 influenza a				
11	590	97.2	121	2	Q6XTK1		Q6xtk1 influenza a				
12	589	97.0	121	2	Q8QJ75		Q8qj75 influenza a				
13	589	97.0	121	2	Q6XTIS		Q6xtis influenza a				
14	589	97.0	121	2	Q6XTI7		Q6xti7 influenza a				
15	588	96.9	121	1	VNS2_IAROM		P03506 influenza a				
16	587	96.7	121	1	VNS2_IACHI		P11619 influenza a				
17	587	96.7	121	2	Q67255		Q67255 influenza a				
18	587	96.7	121	2	Q6KJ5		Q6xtj5 influenza a				
19	587	96.7	121	2	Q777X1		Q777x1 influenza a				
20	586	96.5	121	1	VNS2_IAPOW		P03505 influenza a				
21	586	96.5	121	2	Q697C3		Q693c3 influenza a				
22	586	96.5	121	2	Q6DQJ2		Q6dqj2 influenza a				
23	586	96.5	121	2	Q6DSV1		Q6dsv1 influenza a				
24	586	96.5	121	2	Q612B7		Q612b7 influenza a				
25	586	96.5	121	2	Q6XTC3		Q6xtc3 influenza a				
26	586	96.5	121	2	Q6XTP1		Q6xtp1 influenza a				
27	586	96.5	121	2	Q6XTF3		Q6xtf3 influenza a				
28	586	96.5	121	2	Q6XTF5		Q6xtf5 influenza a				
29	586	96.5	121	2	Q6XTF7		Q6xtf7 influenza a				
30	586	96.5	121	2	Q6XTF9		Q6xtf9 influenza a				
31	586	96.5	121	2	Q6XTG7		Q6xtg7 influenza a				
Scoring table:	BL03DN62										
Gapop 10.0 , Gapext 0.5											
Searched:	1612378 seqs, 512079187 residues										
Total number of hits satisfying chosen parameters:	1612378										
Minimum DB seq length: 0											
Maximum DB seq length: 2000000000											
Post-processing:	Minimum Match 0% Maximum Match 100%										
Listing first 45 summaries											
Database :	UniProt_03_*										
1: uniprot_sprot:*											
2: uniprot_trembl:*											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
Result No.	Score	Query	Match	Length	DB	ID	Description				
1	604	99.5	121	2	Q89733		Q89733 influenza a				
2	600	98.8	121	2	Q67248		Q67248 influenza a				
3	597	98.4	121	1	VNS2_IAUSS		P03504 influenza a				
4	596	98.2	121	2	Q0649		P06049 influenza a				
5	594	97.9	121	1	VNS2_IAANN		P21432 influenza a				
6	594	97.9	121	2	Q6XTU1		Q6xtu1 influenza a				
7	594	97.9	121	2	VNS2_IALB2		P26133 influenza a				
8	590	97.2	121	1	Q67264		Q67264 influenza a				
9	590	97.2	121	2	Q6XTU9		Q6xtu9 influenza a				
10	590	97.2	121	2	Q6XTK1		Q6xtk1 influenza a				
11	590	97.0	121	2	Q8QJ75		Q8qj75 influenza a				
12	589	97.0	121	2	Q6XTIS		Q6xtis influenza a				
13	589	97.0	121	2	Q6XTI7		Q6xti7 influenza a				
14	589	97.0	121	2	Q6XTI7		Q6xti7 influenza a				
15	588	96.9	121	1	VNS2_IAROM		P03506 influenza a				
16	587	96.7	121	1	VNS2_IACHI		P11619 influenza a				
17	587	96.7	121	2	Q67255		Q67255 influenza a				
18	587	96.7	121	2	Q6KJ5		Q6xtj5 influenza a				
19	587	96.7	121	2	Q777X1		Q777x1 influenza a				
20	586	96.5	121	1	VNS2_IAPOW		P03505 influenza a				
21	586	96.5	121	2	Q697C3		Q693c3 influenza a				
22	586	96.5	121	2	Q6DQJ2		Q6dqj2 influenza a				
23	586	96.5	121	2	Q6DSV1		Q6dsv1 influenza a				
24	586	96.5	121	2	Q612B7		Q612b7 influenza a				
25	586	96.5	121	2	Q6XTC3		Q6xtc3 influenza a				
26	586	96.5	121	2	Q6XTP1		Q6xtp1 influenza a				
27	586	96.5	121	2	Q6XTF3		Q6xtf3 influenza a				
28	586	96.5	121	2	Q6XTF5		Q6xtf5 influenza a				
29	586	96.5	121	2	Q6XTF7		Q6xtf7 influenza a				
30	586	96.5	121	2	Q6XTF9		Q6xtf9 influenza a				
31	586	96.5	121	2	Q6XTG7		Q6xtg7 influenza a				
Scoring table:	BL03DN62										
Gapop 10.0 , Gapext 0.5											
Searched:	1612378 seqs, 512079187 residues										
Total number of hits satisfying chosen parameters:	1612378										
Minimum DB seq length: 0											
Maximum DB seq length: 2000000000											
Post-processing:	Minimum Match 0% Maximum Match 100%										
Listing first 45 summaries											
Database :	UniProt_03_*										
1: uniprot_sprot:*											
2: uniprot_trembl:*											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											

Q67248 PRELIMINARY; PRT; 121 AA.  
 AC Q67248\_1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Non-structural protein.  
 GN Name=NS2;  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A. PubMed=7483294;  
 RX MEDLINE=96082767; PubMed=7483294;  
 RA Ward A.C., Azad A.A., McKimm-Breschkin J.L.;  
 RT "Changes in the NS gene of neurovirulent strains of influenza affect  
 RT splicing.";  
 RL Virus Genes 10:91-94 (1995).  
 DR EMBL; L25730; AAA91339.1; -.  
 DR PDB; 1PDB; X-ray; A/B59-116.  
 GO; GO:0010102; C:virion; IBA.  
 DR InterPro; IPR00968; Flu\_NS2.  
 DR Pfam; PF00601; Flu\_NS2; I.  
 KW Non-structural protein.  
 SQ SEQUENCE 121 AA; 14326 MW; B15C197E22F8E294 CRC64;  
 Query Match 98.8%; Score 600; DB 2; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 1.3e-43;  
 Matches 119; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 4  
 Q06049 PRELIMINARY; PRT; 121 AA.  
 ID Q06049; AC Q06049; DR 01-NOV-1996 (TREMBLrel. 01, Created)  
 DR 01-MAR-1996 (TREMBLrel. 01, Last sequence update)  
 DR 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DR Non-structural protein 1.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A. PubMed=8502573;  
 RX MEDLINE=9275765;  
 RA Ward A.C., Azad A.A., Macreadie I.G., McKimm-Breschkin J.L.;  
 RT "Complete nucleotide sequence of the non-structural gene of the human  
 Influenza virus strain A/Ws/33.";  
 RL Nucleic Acids Res. 21:2257-2257(1993).  
 DR EMBL; Z21498; CAA79707.1; -.  
 DR PIR; S33685; DR  
 DR InterPro; IPR00968; Flu\_NS2.  
 DR Pfam; PF00601; Flu\_NS2; I.  
 SQ SEQUENCE 121 AA; 14399 MW; B15C16C794F75B22 CRC64;  
 Query Match 98.2%; Score 596; DB 2; Length 121;  
 Best Local Similarity 98.3%; Pred. No. 2.8e-43;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 5  
 VNS2\_IAUSS STANDARD; PRT; 121 AA.  
 ID P03504; AC P03504; DR 21-JUL-1986 (Rel. 01, Created)  
 DR 05-JUL-1986 (Rel. 44, Last sequence update)  
 DR 05-JUL-2004 (Rel. 44, Last annotation update)  
 DB Non-structural protein NS2.  
 GN Names; Synonyms=8;  
 OS Influenza A virus (strain A/US/90/77 H1N1).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxID=2250033;  
 RN [1]  
 RP SEQUENCE FROM N.A. PubMed=83164298;  
 RX MEDLINE=83164298; PubMed=6834468;  
 RA Krystal M., Buonagurio D.A., Young J.F., Palese P.;  
 RT "Sequential mutations in the NS genes of influenza virus field  
 strains";  
 RL J. Virol. 45:547-554 (1983).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=NS2;  
 CC IsoID=PF03504-1; Sequence=Displayed;  
 CC Name=NS1;  
 CC IsoID=PF03498-1; Sequence=External;  
 CC SEQUENCE FROM N.A. PubMed=6834468;  
 CC Krystal M., Buonagurio D.A., Young J.F., Palese P.;  
 CC "Sequential mutations in the NS genes of influenza virus field  
 strains";  
 CC Name=NS2;  
 CC IsoID=PF03504-1; Sequence=Displayed;  
 CC Name=NS1;  
 CC SEQUENCE FROM N.A. PubMed=6834468;  
 CC Krystal M., Buonagurio D.A., Young J.F., Palese P.;  
 CC "Sequential mutations in the NS genes of influenza virus field  
 strains";  
 CC Name=NS2;  
 CC IsoID=PF03504-1; Sequence=Displayed;  
 CC Name=NS1;



SEQUENCE FROM N. A.  
 MEDLINE=912/2515; PubMed=2053297;  
 RX Schultz U., Fitch W.M., Ludwig S., Mandl J., Scholtissek C.;  
 RA "Evolution of pig influenza viruses.";  
 RT Virology 183 (61-73 (1991).  
 RL DR EMBL; NS5484; AAA43498.1;  
 DR GO; GO-0019012; C-virion; IEA.  
 DR GO; GO-0003723; P:RNA binding; IEA.  
 DR InterPro; IPR000536; Flu NS1.  
 DR InterPro; IPR000668; Flu NS2.  
 DR Pfam; PF00600; Flu\_NS1; I.  
 DR Pfam; PF00601; Flu\_NS2; I.  
 DR Nonstructural protein.  
 KW SEQUENCE 121 AA; 14349 MW; F472EE29D7D471C6F CRC64;  
 SQ

SEQUENCE FROM N. A.  
 MEDLINE=22124158; PubMed=1733114;  
 RX Klimov A.I., Cox N.J., Yotov W.V., Rocha E., Alexandrova G.I.,  
 RA Kendal A.P.;  
 RA "Sequence changes in the live attenuated, cold-adapted variants of  
 influenza A/Leipzig/134/57 (H2N2) virus.";  
 RT "Sequence changes in the live attenuated variants of  
 influenza A/Leipzig/134/57 (H2N2) virus.";  
 DR I- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=2;  
 Name=NS2;  
 IsoID=P261331-1; Sequence=Displayed;  
 Name=NS1;  
 IsoID=P26131-1; Sequence=External;

RESULT 10  
 Q6XT19 PRELIMINARY;  
 ID Q6XT19  
 AC Q6XT19  
 DR 05-JUL-2004 (TREMBLrel. 27, Created)  
 DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DR Non-structural protein NS2.  
 DR Influenza A virus (A/Albany/6/58 (H2N2)).  
 OC Viruses: ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A; H2N2 subtype.  
 RN SEQUENCE FROM N. A.  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY210157; AA046580.1;  
 DR InterPro; IPR000668; Flu\_NS2.  
 DR Pfam; PF00601; Flu\_NS2; I.  
 DR Sequence: DB9C1D2C64DC9E32 CRC64;  
 DR SEQUENCE 121 AA; 14350 MW; DB9C1D2C64DC9E32 CRC64;

Query Match 97.2% Score 590; DB 1; Length 121;  
 Best Local Similarity 95.9%; Pred. No. 9e-43;  
 Matches 116; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Q6XT19 PRELIMINARY;  
 ID Q6XT19  
 AC Q6XT19  
 DR 05-JUL-2004 (TREMBLrel. 27, Created)  
 DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DR Non-structural protein NS2.  
 DR Influenza A virus (A/Albany/6/58 (H2N2)).  
 OC Viruses: ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A; H2N2 subtype.  
 RN SEQUENCE FROM N. A.  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY210157; AA046580.1;  
 DR InterPro; IPR000668; Flu\_NS2.  
 DR Pfam; PF00601; Flu\_NS2; I.  
 DR Sequence: DB9C1D2C64DC9E32 CRC64;  
 DR SEQUENCE 121 AA; 14350 MW; DB9C1D2C64DC9E32 CRC64;

Query Match 97.2% Score 590; DB 2; Length 121;  
 Best Local Similarity 95.9%; Pred. No. 9e-43;  
 Matches 116; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Q6XT19 PRELIMINARY;  
 ID Q6XT19  
 AC Q6XT19  
 DR 05-JUL-2004 (TREMBLrel. 27, Created)  
 DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DR Non-structural protein NS2.  
 DR Influenza A virus (A/Albany/6/58 (H2N2)).  
 OC Viruses: ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A; H2N2 subtype.  
 RN SEQUENCE FROM N. A.  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY210157; AA046580.1;  
 DR InterPro; IPR000668; Flu\_NS2.  
 DR Pfam; PF00601; Flu\_NS2; I.  
 DR Sequence: DB9C1D2C64DC9E32 CRC64;

Query Match 97.2% Score 590; DB 1; Length 121;  
 Best Local Similarity 95.9%; Pred. No. 9e-43;  
 Matches 116; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Q6XT19 PRELIMINARY;  
 ID Q6XT19  
 AC Q6XT19  
 DR 05-JUL-2004 (TREMBLrel. 01, Created)  
 DR 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DR 01-NOV-1996 (TREMBLrel. 01, Last annotation update)  
 DR Non-structural protein 2.  
 DR Name=NS2;  
 DR Influenza A virus.  
 OC Viruses: ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A.  
 RN SEQUENCE FROM N. A.  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY210157; AA046580.1;  
 DR InterPro; IPR000668; Flu\_NS2.  
 DR Pfam; PF00601; Flu\_NS2; I.  
 DR Sequence: DB9C1D2C64DC9E32 CRC64;

RESULT 9  
 Q67264 PRELIMINARY;  
 ID Q67264  
 AC Q67264  
 DR 01-NOV-1996 (TREMBLrel. 01, Created)  
 DR 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DR 01-NOV-1996 (TREMBLrel. 01, Last annotation update)  
 DR Non-structural protein 2.  
 DR Name=NS2;  
 DR Influenza A virus.  
 OC Viruses: ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A.  
 RN SEQUENCE FROM N. A.  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY210157; AA046580.1;  
 DR InterPro; IPR000668; Flu\_NS2.  
 DR Pfam; PF00601; Flu\_NS2; I.  
 DR Sequence: DB9C1D2C64DC9E32 CRC64;

Q6XTK1;	61	RNGKWRQLGKPFEEIRWLLIEVRHRLKITENSFEQTITOPESLKLRYDSDLGAVMRGDLHLSQLN	120
DT 05-JUL-2004 (TREMBLrel. 27, Created)	QY	61 RNGKWRQLGKPFEEIRWLLIEVRHRLKITENSFEQTITOPESLKLRYDSDLGAVMRGDLHLSQLN	120
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	Db	61 RNGKWRQLGKPFEEIRWLLIEVRHRLKITENSFEQTITOPESLKLRYDSDLGAVMRGDLHLSQLN	120
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	QY	121 1 121	
DB Non-structural protein NS2.	Db	121 1 121	
OS Influenza A virus (strain A/Singapore/1/57 H2N2).	QY		
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;			
OC Influenzavirus A; H2N2 subtype.			
OX NCBI_TaxID=220949;			
RN [1]			
SEQUENCE FROM N.A.			
RP Lindstrom S.E., Cox N.J., Klimov A.;			
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
RL DR InterPro; IPR000968; Flu_NS2.			
DR Pfam; PF0601; Flu_NS2; 1.			
SEQUENCE 121 AA; 14381 MW; DB8C0196C2C02484 CRC64;			
Query Match 97.2%; Score 590; DB 2; Length 121;			
Best Local Similarity 95.9%; Pred. No. 9e-43; Mismatches 3; Conservative 3; Indels 0; Gaps 0;			
Matches 116; Non-structural protein NS2.			
QY 1 MDPNVTSFQDILRKISKMOGLGSSSEDLNGITOPESLKLRYDSDLGAVMRGDLHLSQLN 60			
Db 1 MDPNVTSFQDILRKISKMOGLGSSSEDLNGITOPESLKLRYDSDLGAVMRGDLHLSQLN 60			
DR InterPro; IPR000968; Flu_NS2.			
DR Pfam; PF0601; Flu_NS2; 1.			
SEQUENCE 121 AA; 14339 MW; CB721E67D2D12584 CRC64;			
Query Match 97.0%; Score 589; DB 2; Length 121;			
Best Local Similarity 95.9%; Pred. No. 1.1e-42; Mismatches 3; Conservative 3; Indels 0; Gaps 0;			
Matches 116; Non-structural protein NS2.			
QY 121 1 121			
Db 121 1 121			
RESULT 12			
Q8QLT5			
ID Q8QLT5		PRELIMINARY;	
AC Q8QLT5;		PRT;	121 AA.
DT 01-JUN-2002 (TREMBLrel. 21, Created)			
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DB Non-structural protein NS2.			
GN Name=NS2;			
OS Influenza A virus (A/Swine/Core d'Armor/3633/84 (H3N2)).			
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;			
OC Influenzavirus A; H3N2 subtype.			
OX NCBI_TaxID=164041;			
RN [1]			
SEQUENCE FROM N.A.			
RP STRAIN=A/Swine/Cotes d'Armor/3633/84;			
RC MEDLINE=190432; PubMed=11900321;			
RX Marozin S., Gregory V., Cameron K., Bennett M., Valette M., Aymard M.,			
RA Poni P., Parigazzi G., Lin Y., Hay A.,			
RA "Antigenic and genetic diversity among swine influenza A H1N1 and H1N2 viruses in Europe";			
RT J. Gen. Virol. 83:735-745(2002).			
DR GO:GO:0003723; F RNA binding; IEA.			
DR InterPro; IPR000256; Flu_NS1.			
DR InterPro; IPR000968; Flu_NS2.			
DR Pfam; PF0600; Flu_NS1; 1.			
DR Pfam; PF0601; Flu_NS2; 1.			
SEQUENCE 121 AA; 14330 MW; 149A44531AD7865 CRC64;			
Query Match 97.0%; Score 589; DB 2; Length 121;			
Best Local Similarity 96.7%; Pred. No. 1.1e-42; Mismatches 3; Conservative 3; Indels 0; Gaps 0;			
Matches 117; Non-structural protein NS2.			
QY 1 MDPNVTSFQDILRKISKMOGLGSSSEDLNGITOPESLKLRYDSDLGAVMRGDLHLSQLN 60			
Db 1 MDPNVTSFQDILRKISKMOGLGSSSEDLNGITOPESLKLRYDSDLGAVMRGDLHLSQLN 60			

Dbb	1	MDPATVSSQDILRMSKQLGSSEDINGMTOFESKRLYDSDLGAVMGRGDLHSQN	60
Qy	61	RNGKWRQLGKPPBEIRVLLIEEVHRLKITENSFBOITFMQALQLLVEEQIRTSFSQL	120
Db	61	RNGKWRQLGKPPBEIRVLLIEEVHRLKITENSFBOITFMQALQLLVEEQIRTSFSQL	120
Qy	121	I	121
Db	121	I	121